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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:16:31 ; Search time 38 Seconds

(without alignments)
1570.955 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 448
Sequence: 1 MSOSTQNEFLSPFQHM.....PKSDVFRHRSKPNRSYYP 448

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002.*

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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	448	100.0	448	20	AAV45246	Human p51 protein
2	448	100.0	448	20	AAV05955	Human cell regulat
3	448	100.0	448	21	AAAB11359	Human p63 protein
4	448	100.0	448	22	AAAB2128	Human protein #1 u
5	448	100.0	448	23	ABAB74991	Human p53 homology
6	410	91.5	516	20	AAV05954	Human cell regulat
7	410	91.5	516	21	AAAB11363	Human p53 protein
8	410	91.5	516	23	ABAB74995	Human p53 homology
9	410	91.5	641	20	AAV45247	Human p51 protein
10	410	91.5	641	20	AAV05953	Human cell regulat

11	410	91.5	641	21	AAAB11358	Human p63 protein
12	410	91.5	641	22	AAAB2129	Human protein #2 u
13	410	91.5	641	23	ABAB74990	Human p53 homology
14	410	91.5	680	21	AAAB11361	Human p53 protein
15	410	91.5	680	21	AAV50997	Human KET protein
16	410	91.5	680	23	ABAB74993	Human p53 homology
17	379	84.6	393	20	AAV05957	Human cell regulat
18	341	76.1	461	21	AAAB11362	Human p63 protein
19	341	76.1	461	23	ABAB74994	Human p53 homology
20	341	76.1	586	20	AAV05956	Human cell regulat
21	284	63.4	483	20	AAV05958	Human cell regulat
22	284	63.4	680	20	AAV05958	Human cell regulat
23	272	60.7	586	21	AAAB11357	Human p63 protein
24	272	60.7	586	23	ABAB74989	Human p53 homology
25	269	60.0	356	20	AAV43135	Human p40 protein
26	269	60.0	356	21	AAAB11360	Human p63 protein
27	269	60.0	356	23	ABAB74992	Human p53 homology
28	259	57.8	389	20	AAV05964	Mouse cell regulat
29	259	57.8	461	20	AAV05963	Mouse cell regulat
30	259	57.8	586	20	AAV05962	Mouse cell regulat
31	248	55.4	680	21	AAV50998	Rat KET protein
32	191	42.6	586	20	AAV41032	Human lung tumor a
33	191	42.6	586	21	AAAB11317	Human lung cancer
34	191	42.6	586	23	ABAB74949	Human lung tumor
35	49	10.9	155	20	AAV05960	Mouse cell regulat
36	49	10.9	403	22	AAAB84840	p73 gamma protein
37	49	4.9	475	22	AAAB84839	p73 gamma protein
38	49	4.9	499	18	AAW36190	Human p53 tumor s
39	49	4.9	499	21	AAV44635	Monkey p53 tumor
40	49	4.9	499	21	AAV44635	Human p73 beta spl
41	49	4.9	499	22	AAAB84838	p73 beta protein s
42	49	4.9	506	18	AAW36188	Human p53 tumor s
43	49	4.9	587	18	AAW36187	Human p53 tumor s
44	49	4.9	588	18	AAW36189	Human p53 tumor s
45	49	4.9	635	20	AAW30661	Human NBS-1 alpha

ALIGNMENTS

RESULT 1	
AAV45246	standard; Protein; 448 AA.
AAV45246	
07-JAN-2000	(first entry)
Human p51 protein A.	
Human; p51; p53 related gene; cell proliferation; regulation; cancer;	
tumour suppression; diagnosis.	
Homo sapiens.	
Key	Location/Qualifiers
Domain	1..39
Domain	/label= transactivation_domain
Domain	142..321
Domain	/label= dna_binding_domain
Domain	353..397
Domain	/label= oligomerisation_domain
W09950412-A1.	
07-OCT-1999.	
24-MAR-1999;	99W0-JP01512.
27-MAR-1998;	98JP-0100467.
(SAKA) OTSUKA PHARM CO LTD.	
(IKAWA) IKAWA Y.	

XX Ikawa Y, Ikawa S, Obinata M;
XX
XX WPI: 1999-591318/50.
DR
DR N-PSDB: AAZ25770.
XX

XX New p53 related human gene p51, useful for diagnosis, investigation and
PT treatment of cancers and screening for potential cell proliferation
PT agents -
XX

PS Claim 1; Page 147-148; 163pp; Japanese.
XX

CC The present sequence represents a human p51 protein, which is related to
CC p53 and has cell proliferation regulation and tumour suppression
CC activity. The p51 gene can be used in the investigation, diagnosis and
CC treatment of diseases such as cancer, with which the p53 family cell
CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
XX

SO Sequence 448 AA;

Query Match 100.0%; Score 448; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPFVFOHIMDFLEOPICSVOPIDLNFDVDESDGATNKRIETSMDCIRMO 60
DB 1 MSOSTQTNFELSPFVFOHIMDFLEOPICSVOPIDLNFDVDESDGATNKRIETSMDCIRMO 60
QY 61 DSLSLSDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSSTFDAL 120
DB 61 DSLSLSDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSSTFDAL 120
QY 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
DB 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
QY 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
DB 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
QY 181 POGAVIRAMPYKKAHVTEYVKKRCPNHLSRENEGQIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHVTEYVKKRCPNHLSRENEGQIAPPSHLIRVEGNSHAQYVDP 240
QY 241 ITGROSIVLYPEPOVGTETFTVLYNMCNCSGCVGNRRPILITVLETRDGOVLGRRC 300
DB 241 ITGROSIVLYPEPOVGTETFTVLYNMCNCSGCVGNRRPILITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADSDIRKQOVSSTKNGSGTKRPFQONTHGIONTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADSDIRKQOVSSTKNGSGTKRPFQONTHGIONTSIKRRSPDDE 360
QY 361 LLYIPVGRGTYEMLKIKESLELMQYLPQHTIETRYRQOQOQHILQKHLSACFRNE 420
DB 361 LLYIPVGRGTYEMLKIKESLELMQYLPQHTIETRYRQOQOQHILQKHLSACFRNE 420
QY 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448
DB 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448

RESULT 2

AAI05955

ID AAY05955 standard; Protein; 448 AA.

AC AAY05955;

DT 16-AUG-1999 (first entry)

DE Human cell regulatory protein p63, isoform hUTAP63 gamma.

KW Cell regulatory protein; p63; hUTAP63 gamma; Tap63 gamma; human;

KW cancer; tumour suppressor; cell cycle control; apoptosis;

KW cell proliferation; cell differentiation; therapy.

OS Homo sapiens.

PN WO9919357-A2.

FD 22-APR-1999.

PF 02-OCT-1998; 98WO-US21992.

PR 29-MAY-1998; 98US-0087216.

PR 15-OCT-1997; 97US-0062076.

PA (HARD) HARVARD COLLEGE.

PI McKeon F, Yang A;

DR WPI: 1999-277595/23.

DR N-PSDB: AAX58574.

PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours

PS Claim 23; Fig 11; 161pp; English.

CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to a particular position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p53 members differing in the N-terminus are
CC designated as delta and epsilon forms, where the delta form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isoform Tap63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05955-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

SO Sequence 448 AA;

Query Match 100.0%; Score 448; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPFVFOHIMDFLEOPICSVOPIDLNFDVDESDGATNKRIETSMDCIRMO 60
DB 1 MSOSTQTNFELSPFVFOHIMDFLEOPICSVOPIDLNFDVDESDGATNKRIETSMDCIRMO 60
QY 61 DSLSLSDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSSTFDAL 120
DB 61 DSLSLSDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSSTFDAL 120
QY 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
DB 121 SPSPAIPSNIDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVWTPP 180
QY 181 POGAVIRAMPYKKAHVTEYVKKRCPNHLSRENEGQIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHVTEYVKKRCPNHLSRENEGQIAPPSHLIRVEGNSHAQYVDP 240

QY 241 ITGRQSVLVPEPQVGTETFTVLYNFMCNSSCVGMNRRPILITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLVPEPQVGTETFTVLYNFMCNSSCVGMNRRPILITVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTAKRPFONTGIGIOMTSIKRRSPDDE 360
 DB 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTAKRPFONTGIGIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOQOQHLLQKHLISACPRNE 420
 DB 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOQOQHLLQKHLISACPRNE 420
 QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 DB 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 RESULT 3
 ID AAB11359 standard; protein: 448 AA.
 AC AAB11359;
 DT 21-FEB-2001 (first entry)
 DE Human p63 protein isoform #3.
 KM Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.
 OS Homo sapiens.
 XX MO200061612-A2.
 XX 19-OCT-2000.
 XX 03-APR-2000; 2000WO-US08896.
 XX 02-APR-1999; 99US-0285479.
 XX 17-DEC-1999; 99US-0466396.
 XX 30-DEC-1999; 99US-0476496.
 XX 10-JAN-2000; 2000US-0480884.
 XX 22-FEB-2000; 2000US-0510376.
 XX (CORI-) CORIXA CORP.
 XX Wang T, Fan L;
 XX WPI: 2000-628399/60.
 XX N-PSDB: AAC66029.
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 PS Disclosure; Page 247-249; 261pp; English.
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX Sequence 448 AA;
 SQ Query Match 100.0%; Score 448; DB 21; Length 448;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSQTQNEFLSPEVQEHIMDFEQIPCSVQPIDLNFVDEPSEDGATKIEISMDCIIMQ 60
 DB 1 MSQTQNEFLSPEVQEHIMDFEQIPCSVQPIDLNFVDEPSEDGATKIEISMDCIIMQ 60
 QY 61 DSDLSDPMMPOYTMGLINSMDQOIONGSSSTSEYNTDHAONSTYAPSPYAPSSSTDAL 120
 DB 61 DSDLSDPMMPOYTMGLINSMDQOIONGSSSTSEYNTDHAONSTYAPSPYAPSSSTDAL 120
 QY 121 SPSPAIISNTDYPPPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIISNTDYPPPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 PGAVIRAMPYKKAHEVTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 DB 181 PGAVIRAMPYKKAHEVTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGRQSVLVPEPQVGTETFTVLYNFMCNSSCVGMNRRPILITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLVPEPQVGTETFTVLYNFMCNSSCVGMNRRPILITVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTAKRPFONTGIGIOMTSIKRRSPDDE 360
 DB 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTAKRPFONTGIGIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOQOQHLLQKHLISACPRNE 420
 DB 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOQOQHLLQKHLISACPRNE 420
 QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 DB 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 RESULT 4
 ID AAB82128 standard; protein: 448 AA.
 AC AAB82128;
 DT 03-AUG-2001 (first entry)
 DE Human protein #1 used to produce a chimeric p53 protein.
 KM Human; cytostatic; gene therapy; p53; human tumour.
 KW Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 XX Domain 1..59
 XX Domain /label= Transactivation_domain
 XX Domain 142..321
 XX Domain /label= DNA_binding_domain
 XX Domain 353..397
 XX Domain /label= Oligomerisation_domain
 XX JP200035448-A.
 XX 26-DEC-2000.
 XX 09-APR-1999; 99JP-0139034.
 XX 09-APR-1999; 99JP-0139034.
 XX (IKAWA/) IKAWA H.
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX WPI: 2001-268293/28.
 XX N-PSDB: AAF65588.
 PT Chimera gene of the p53 family, useful for gene therapy, and treatment

PT of cancer, comprises a transcription activating region and a DNA
 binding region -

Example 1; Page 30-32; 57pp: Japanese.

CC The present invention relates to a chimera gene of p53 family encoding a
 CC transcription activating region, a DNA binding region, and an oligomer
 CC formation region of different p53 family proteins. The chimera gene can
 CC be used for gene therapy of p53 variant human tumours, and analysis of
 CC the function of the p53 family gene. The present sequence was used in the
 CC present invention.

CC Sequence 448 AA:

Query Match 100.0%; Score 448; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTEFEFSPEFHQIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
 DB 1 MSOSTQTEFEFSPEFHQIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
 QY 61 DSDLSDPMPQYTNIGLNSMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNIGLNSMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKWTTP 180
 DB 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKWTTP 180
 QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVGENSHQAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVGENSHQAQYVEDP 240
 QY 241 ITGQOSVLYVEPPQVGTETFTVLYNFMCSNCSGVGNNRRPILITLTETRDGOVYGRRC 300
 DB 241 ITGQOSVLYVEPPQVGTETFTVLYNFMCSNCSGVGNNRRPILITLTETRDGOVYGRRC 300
 QY 301 FEARICACPGDRKADSDSIRKQOVSSTKNGDGTAKRPFRONTNHIOMTSIKRRSPDDE 360
 DB 301 FEARICACPGDRKADSDSIRKQOVSSTKNGDGTAKRPFRONTNHIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFENE 420
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFENE 420
 QY 421 LVEPRRETPOKSDVFFRHSKPPNRSYYP 448
 DB 421 LVEPRRETPOKSDVFFRHSKPPNRSYYP 448

RESULT 5
 ABB74991
 ID ABB74991 standard; Protein; 448 AA.
 AC ABB74991.

DT 01-MAY-2002 (first entry)

DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:340.

KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 immune response.

OS Homo sapiens.

XX WO200200174-A2.

PN 03-JAN-2002.

PD 28-JUN-2001; 2001WO-US21065.

PF 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

PI Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MM, Marnetakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

DR WPI; 2002-090513/12.
 DR N-PSDB; ABL49248.

PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 PS Example 2; Page 322-323; 374pp; English.

CC The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

SO Sequence 448 AA:

Query Match 100.0%; Score 448; DB 23; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTEFEFSPEFHQIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
 DB 1 MSOSTQTEFEFSPEFHQIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
 QY 61 DSDLSDPMPQYTNIGLNSMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNIGLNSMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKWTTP 180
 DB 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKWTTP 180
 QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVGENSHQAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVGENSHQAQYVEDP 240
 QY 241 ITGQOSVLYVEPPQVGTETFTVLYNFMCSNCSGVGNNRRPILITLTETRDGOVYGRRC 300
 DB 241 ITGQOSVLYVEPPQVGTETFTVLYNFMCSNCSGVGNNRRPILITLTETRDGOVYGRRC 300
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 DB 301 FEARICACPGDRKADSDSIRKQOVSSTKNGDGTAKRPFRONTNHIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFENE 420
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFENE 420
 QY 421 LVEPRRETPOKSDVFFRHSKPPNRSYYP 448
 DB 421 LVEPRRETPOKSDVFFRHSKPPNRSYYP 448

RESULT 6
 AA05954
 ID AA05954 standard; Protein; 516 AA.

XX AAY05954;
 XX 16-AUG-1999 (first entry)
 XX
 DE Human cell regulatory protein p63, isoform hUTAP63 beta.
 DE
 KW Cell regulatory protein: p63; hUTAP63 beta; TAP63 beta; human;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO9919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PF 02-OCT-1998; 98WO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 PI
 PI McKeon F, Yang A;
 XX
 DR WPI: 1999-277595/23.
 DR N-PSDB: AAY58573.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 10; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform TAP63 beta. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAY58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 SO Sequence 516 AA;

Query Match 91.5%; Score 410; DB 20; Length 516;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQNEFLSPVFOHIMFLPQICSVOPIDLNFDVDEPSEGGATKIKISMDICIMQ 60
 DB 1 MSOSTQNEFLSPVFOHIMFLPQICSVOPIDLNFDVDEPSEGGATKIKISMDICIMQ 60

OY DSDLSDDPMPOYTNGLNSMDQOIONSSSTSPYNTDHAONSTAPSPYAPSSSTPDAL 120
 DB 61 DSDLSDDPMPOYTNGLNSMDQOIONSSSTSPYNTDHAONSTAPSPYAPSSSTPDAL 120
 OY 121 SPSPAPISNTDYPGPHSFDSVFOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
 DB 121 SPSPAPISNTDYPGPHSFDSVFOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
 OY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHLSREFNEGIIAPPSHLIRVGNSHQYVDP 240
 DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHLSREFNEGIIAPPSHLIRVGNSHQYVDP 240
 OY 241 ITGRSVLPVPEPPQVGTFTTLYNFMCNSSCVGAMRRPILITVLETBDGVLGRRC 300
 DB 241 ITGRSVLPVPEPPQVGTFTTLYNFMCNSSCVGAMRRPILITVLETBDGVLGRRC 300
 OY 301 FEARICACPGDRRADEDSIRKQVSDSTKNGDGRKRPFRONTGHIQMTSIRKRRSPDE 360
 DB 301 FEARICACPGDRRADEDSIRKQVSDSTKNGDGRKRPFRONTGHIQMTSIRKRRSPDE 360
 OY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHHLQK 410
 DB 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHHLQK 410

RESULT 7
 AAB11363
 ID AAB11363 standard; Protein: 516 AA.

AAB11363;

21-FEB-2001 (first entry)

Human p63 protein isoform #7.

Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 vaccine; detection.

Homo sapiens.

WO200061612-A2.

19-OCT-2000.

03-APR-2000; 2000WO-US08896.

02-APR-1999; 99US-0285479.

17-DEC-1999; 99US-0466396.

30-DEC-1999; 99US-0476496.

10-JAN-2000; 2000US-0480884.

22-FEB-2000; 2000US-0510376.

(CORI-) CORIXA CORP.

Mang T, Fan L;

WPI: 2000-628399/60.

N-PSDB: AAC66033.

Isolated polypeptide comprising an immunogenic portion of a lung tumor
 protein is used for detecting and monitoring progression of lung cancer
 in a patient -

Disclosure; Page 255-256; 261pp; English.

This invention describes a novel isolated polypeptide (I) which
 comprising an immunogenic portion of a lung tumor protein or variant (P2)
 which have cytostatic activity. The polypeptides and polynucleotides are
 used in compositions and vaccines to inhibit the development of cancer,
 especially lung cancer, in a patient. Methods described in the invention
 can be used to monitor the progression of a cancer by carrying out the
 detection at subsequent time points and comparing the results from a patient
 different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

CC are treated with p2, polynucleotides encoding p2 or antigen presenting
 CC cells expressing p2 and then administered to the patient to inhibit
 CC development of cancer.

Sequence 516 AA:

Query Match 91.5%; Score 410; DB 21; Length 516;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFLESEVFOHIMDFLEQPCISVOPIDLFNFDSESDGATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNFLESEVFOHIMDFLEQPCISVOPIDLFNFDSESDGATNKIEISMDCIRMQ 60
 QY 61 DSDLSDPMPQYNTNGLNSMDQOIONGSSSTPYNTDHAONSVTAAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYNTNGLNSMDQOIONGSSSTPYNTDHAONSVTAAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNSTDYPGHSHFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 DB 121 SPSPAIPSNSTDYPGHSHFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 QY 181 PGAVIRAMPYKKAHEHTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 PGAVIRAMPYKKAHEHTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGRQSVLVPEPPQVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRRC 300
 DB 241 ITGRQSVLVPEPPQVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTAKPRFRQNHGIQMTSIRKRRSPDDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTAKPRFRQNHGIQMTSIRKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQK 410
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQK 410

RESULT 8
 ABB74995.
 ID ABB74995 standard; Protein: 516 AA.

XX AC ABB74995;
 XX DT 01-MAY-2002 (first entry)
 XX DE Human p53 homologue isoform, p53 (L530S) protein SEQ ID NO:344.
 XX KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 XX OS Immune response.
 XX OS Homo sapiens.
 XX PN WO200200174-A2.
 XX PD 03-JAN-2002.
 XX PF 28-JUN-2001; 2001MO-US21065.
 XX PR 28-JUN-2000; 2000US-0606421.
 XX PR 02-AUG-2000; 2000US-0630940.
 XX PR 21-AUG-2000; 2000US-0643597.
 XX PR 15-SEP-2000; 2000US-0662786.
 XX PR 09-OCT-2000; 2000US-0685696.
 XX PR 12-DEC-2000; 2000US-0735705.
 XX PR 07-MAY-2001; 2001US-0850716.
 XX PA (CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Reltier MW, Marnierakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI: 2002-090513/12.
 DR N-PSDB: ABL49252.

PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 PS Example 2; Page 327-328; 374pp; English.

CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

Sequence 516 AA:

Query Match 91.5%; Score 410; DB 23; Length 516;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFLESEVFOHIMDFLEQPCISVOPIDLFNFDSESDGATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNFLESEVFOHIMDFLEQPCISVOPIDLFNFDSESDGATNKIEISMDCIRMQ 60
 QY 61 DSDLSDPMPQYNTNGLNSMDQOIONGSSSTPYNTDHAONSVTAAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYNTNGLNSMDQOIONGSSSTPYNTDHAONSVTAAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNSTDYPGHSHFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 DB 121 SPSPAIPSNSTDYPGHSHFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 QY 181 PGAVIRAMPYKKAHEHTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 PGAVIRAMPYKKAHEHTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGRQSVLVPEPPQVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRRC 300
 DB 241 ITGRQSVLVPEPPQVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTAKPRFRQNHGIQMTSIRKRRSPDDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTAKPRFRQNHGIQMTSIRKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQK 410
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQK 410

RESULT 9
 AAY45247
 ID AAY45247 standard; Protein: 641 AA.

XX AC AAY45247;
 XX DT 07-JAN-2000 (first entry)
 XX DE Human p51 protein B.
 XX KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;
 XX OS tumour suppression; diagnosis.
 XX OS Homo sapiens.

FT Key Location/Qualifiers
 FT Domain 1..59
 FT /label= transactivation_domain
 FT Domain 142..321


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Db      61 DSDLSDPMPQYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
OY      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
OY      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
OY      241 ITGROSIVLYPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLRRC 300
Db      241 ITGROSIVLYPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLRRC 300
OY      301 FEARICACPGDRKADDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDE 360
Db      301 FEARICACPGDRKADDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDE 360
OY      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQHHLQK 410
Db      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQHHLQK 410

RESULT 11
AAB11358
ID      AAB11358 standard; protein; 641 AA.
AC      AAB11358;
DT      21-FEB-2001 (first entry)
DE      Human p63 protein isoform #2.
KW      Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW      vaccine; detection.
OS      Homo sapiens.
PN      WO200061612-A2.
PD      19-OCT-2000.
PF      03-APR-2000; 2000WO-US08896.
PR      02-APR-1999; 99US-0285479.
PR      17-DEC-1999; 99US-0466396.
PR      30-DEC-1999; 99US-0476496.
PR      10-JAN-2000; 2000US-0480884.
PR      22-FEB-2000; 2000US-0510376.
PA      (CORI-) CORIXA CORP.
XX      Wang T, Fan L;
XX      WPI; 2000-628399/60.
XX      N-PSDB; AAC66028.
PT      Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT      protein is used for detecting and monitoring progression of lung cancer
PT      in a patient.
XX      Disclosure; Page 245-247; 261pp; English.
XX      This invention describes a novel isolated polypeptide (I) which
XX      comprising an immunogenic portion of a lung tumor protein or variant (P2)
XX      which have cytostatic activity. The polypeptides and polynucleotides are
XX      used in compositions and vaccines to inhibit the development of cancer,
XX      especially lung cancer, in a patient. Methods described in the invention
XX      can be used to monitor the progression of a cancer by carrying out the
XX      detection at subsequent time points and comparing the results from the
XX      different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
XX      are treated with P2, polynucleotides encoding P2 or antigen presenting

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CC      Cells expressing P2 and then administered to the patient to inhibit
CC      development of cancer.
SQ      Sequence 641 AA;
Query Match      91.5%; Score 410; DB 21; Length 641;
Best local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 MSOSTQTNFELSPVEFOHIMDFLEQPCISVQPIDLNFVDPSPDGAATNKIEIMDCIRMQ 60
Db      1 MSOSTQTNFELSPVEFOHIMDFLEQPCISVQPIDLNFVDPSPDGAATNKIEIMDCIRMQ 60
OY      61 DSDLSDPMPQYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db      61 DSDLSDPMPQYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
OY      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
OY      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
OY      241 ITGROSIVLYPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLRRC 300
Db      241 ITGROSIVLYPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLRRC 300
OY      301 FEARICACPGDRKADDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDE 360
Db      301 FEARICACPGDRKADDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDE 360
OY      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQHHLQK 410
Db      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQHHLQK 410

RESULT 12
AAB82129
ID      AAB82129 standard; protein; 641 AA.
AC      AAB82129;
DT      03-AUG-2001 (first entry)
DE      Human protein #2 used to produce a chimeric p53 protein.
KW      Human; cytostatic; gene therapy; p53; human tumour.
OS      Homo sapiens.
XX      Key
XX      Location/Qualifiers
XX      1..59
XX      Domain
XX      /label= Transactivation_domain
XX      142..321
XX      Domain
XX      /label= DNA_binding_domain
XX      353..397
XX      /label= Oligomerisation_domain
XX      JP2000354488-A.
XX      26-DEC-2000.
XX      09-APR-1999; 99JP-0139034.
XX      09-APR-1999; 99JP-0139034.
XX      (IKAWA/) IKAWA H.
XX      (SAKA) OTSUKA PHARM CO LTD.
XX      WPI; 2001-268293/28.
XX      N-PSDB; AAF86589.

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XX Chimera gene of the p53 family, useful for gene therapy, and treatment
 PT of cancer, comprises a transcription activating region and a DNA
 PT binding region -

PS Example 1; Page 37-40; 57pp; Japanese.

XX The present invention relates to a chimera gene of p53 family encoding a
 CC transcription activating region, a DNA binding region, and an oligomer
 CC formation region of different p53 family proteins. The chimeric gene can
 CC be used for gene therapy of p53 variant human tumours, and analysis of
 CC the function of the p53 family gene. The present sequence was used in the
 CC present invention.

XX Sequence 641 AA;

Query Match 91.5%; Score 410; DB 22; Length 641;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPYFQHIWDLFQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 DB 1 MSQSTQTNFELSPYFQHIWDLFQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 QY 61 DSDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSPSTFDAL 120
 DB 61 DSDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSPSTFDAL 120
 QY 121 SPSPAIPSNITDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIATCPQIKVMP 180
 DB 121 SPSPAIPSNITDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIATCPQIKVMP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300
 DB 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
 QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETIYRQOQOQHHLQK 410
 DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETIYRQOQOQHHLQK 410

RESULT 13

ABB74990 ID ABB74990 standard; Protein: 641 AA.

XX ABB74990;

DT 01-MAY-2002 (first entry)

DE Human p53 homologue isoform, p63 (L530S). protein SEQ ID NO:339.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KW immune response.

XX Homo sapiens.

XX MO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MW, Marinakis M, Fanger GR;

PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

DR MPI: 2002-090513/12.

DR N-PDB: ABL49247.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

PS Example 2; Page 321-322; 374pp; English.

XX The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 641 AA;

Query Match 91.5%; Score 410; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPYFQHIWDLFQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 DB 1 MSQSTQTNFELSPYFQHIWDLFQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 QY 61 DSDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSPSTFDAL 120
 DB 61 DSDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSPSTFDAL 120
 QY 121 SPSPAIPSNITDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIATCPQIKVMP 180
 DB 121 SPSPAIPSNITDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIATCPQIKVMP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300
 DB 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
 QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETIYRQOQOQHHLQK 410
 DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETIYRQOQOQHHLQK 410

RESULT 14

AAB11361 ID AAB11361 standard; Protein: 680 AA.

XX AAB11361;

XX 21-FEB-2001 (first entry)

XX Human p63 protein isoform #5.

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.
 XX Homo sapiens.
 OS WO200061612-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000WO-US08896.
 XX
 PR 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Fan L;
 XX
 DR WPI: 2000-628399/60.
 DR N-PSDB; AAC66031.
 XX
 XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient.
 XX
 PS Disclosure; Page 250-253; 261pp; English.
 XX
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC especially in compositions and vaccines to inhibit the development of cancer,
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 CC
 SQ Sequence 680 AA;
 Query Match 91.5%; Score 410; DB 21; Length 680;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMQ 60
 DB 40 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMQ 99
 QY 61 DSDLDSPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 100 DSDLDSPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
 QY 121 SPSPALPSNTDYGPHSFDFVSFQOOSTAKSATWTYTELKLKLYCOIAKTCPIQIKVWTPP 180
 DB 160 SPSPALPSNTDYGPHSFDFVSFQOOSTAKSATWTYTELKLKLYCOIAKTCPIQIKVWTPP 219
 QY 181 PGCAVIRAMPVYKKAHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGSHAOYVDP 240
 DB 220 PGCAVIRAMPVYKKAHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGSHAOYVDP 279
 QY 241 ITGRQSVLVPYEPPOVGETFTVLNFMQNSSCVCGANRRPILIVTLETEDGOVLGRRC 300
 DB 280 ITGRQSVLVPYEPPOVGETFTVLNFMQNSSCVCGANRRPILIVTLETEDGOVLGRRC 339
 QY 301 FEARICACGRKRAKDEDSIRKQOVSDFKNGDGTKRPFRONTAGIQWTSTIKRRSPDDE 360
 DB 340 FEARICACGRKRAKDEDSIRKQOVSDFKNGDGTKRPFRONTAGIQWTSTIKRRSPDDE 399

QY 361 LLYDPVGRRETYEMLKIKESLELMQYLPQRTIETFRQOQOQOHQHLQK 410
 DB 400 LLYDPVGRRETYEMLKIKESLELMQYLPQRTIETFRQOQOQOHQHLQK 449
 RESULT 15
 AA50997
 ID AA50997 standard; Protein; 680 AA.
 XX
 AC AA50997;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human KET protein.
 XX
 KW KET, anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;
 KW p53 family; angiogenic; cytotoxic; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9961610-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 25-MAY-1999; 99WO-DE01557.
 XX
 PR 25-MAY-1998; 98DE-1022985.
 XX
 PA (FRAU) FRAUNHOFER GES FORDERUNG ANGEMANDTEN.
 XX
 PI Paul D, Augustin M, Schmale H, Bamberger C;
 XX
 DR WPI: 2000-062710/05.
 DR N-PSDB; AA43913.
 XX
 PT New KET-encoding nucleic acid and related proteins, for diagnosis and
 PT treatment of tumors.
 XX
 PS Claim 7; Page 26-28; 28pp; German.
 XX
 CC This invention describes a novel KET-encoding nucleic acid (I) and its
 CC fragments, variants and mutants which has anticancer activity. (I)
 CC encodes a protein, (II), involved in control of the cell cycle and
 CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
 CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
 CC detect (I) in biological samples, specifically angiogenic tumor tissue,
 CC including (I) sequences that have a homozygotic deletion and (b) to
 CC detect presence or absence of human chromosome 3q27 or murine chromosome
 CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor
 CC suppressor, particularly in tumors where an alteration in the wild-type
 CC p53 allele has not been identified. (I) and (II) may also be used for
 CC development of specific cytotoxic agents and for predicting the risk of
 CC developing cancer. This sequence represents the human KET protein
 CC described in the method of the invention.
 CC
 SQ Sequence 680 AA;
 Query Match 91.5%; Score 410; DB 21; Length 680;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMQ 60
 DB 40 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMQ 99
 QY 61 DSDLDSPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 100 DSDLDSPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
 QY 121 SPSPALPSNTDYGPHSFDFVSFQOOSTAKSATWTYTELKLKLYCOIAKTCPIQIKVWTPP 180
 DB 160 SPSPALPSNTDYGPHSFDFVSFQOOSTAKSATWTYTELKLKLYCOIAKTCPIQIKVWTPP 219

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OY 181 POGAVIRAMPVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
    |||||||
DB 220 POGAVIRAMPVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
    |||||||
OY 241 ITGROSVALVPEPPPOVGETTEVTLYNFMCNSSCVGGMNRRPILIIYVLETRDQVGLGRRC 300
    |||||||
DB 280 ITGROSVALVPEPPPOVGETTEVTLYNFMCNSSCVGGMNRRPILIIYVLETRDQVGLGRRC 339
    |||||||
OY 301 FEARICACPRGRKADSDSIRKQVSDSTKNGDGTTRPFRONTNGIOMTSIKKRRSPDDE 360
    |||||||
DB 340 FEARICACPRGRKADSDSIRKQVSDSTKNGDGTTRPFRONTNGIOMTSIKKRRSPDDE 399
    |||||||
OY 361 LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETTYRQOQOQOHOHLQK 410
    |||||||
DB 400 LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETTYRQOQOQOHOHLQK 449
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Search completed: June 24, 2003, 22:25:49
 Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2003, 22:11:01 ; Search time 26 Seconds
(without alignments)
1864.487 Million cell updates/sec

Title: US-09-670-568B-1
Perfect score: 448
Sequence: 1 MSQSTQTNFSLPEVFGH.....PKQSDVFRHSPNRSVYP 448

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 417779 seqs, 108206813 residues

Word size : 0

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	448	10	US-09-735-705-340
2	448	100.0	448	10	US-09-850-716A-340
3	448	100.0	448	10	US-09-897-778-340
4	410	91.5	516	10	US-09-735-705-344
5	410	91.5	516	10	US-09-850-716A-344
6	410	91.5	516	10	US-09-897-778-344
7	410	91.5	641	10	US-09-735-705-339
8	410	91.5	641	10	US-09-850-716A-339
9	410	91.5	641	10	US-09-897-778-339
10	410	91.5	680	10	US-09-735-705-342
11	410	91.5	680	10	US-09-850-716A-342
12	410	91.5	680	10	US-09-897-778-342
13	341	76.1	461	10	US-09-735-705-343
14	341	76.1	461	10	US-09-850-716A-343
15	341	76.1	461	10	US-09-897-778-343
16	272	60.7	586	10	US-09-735-705-338
17	272	60.7	586	10	US-09-850-716A-338
18	272	60.7	586	10	US-09-897-778-338
19	269	60.0	356	10	US-09-735-705-341

20	269	60.0	356	10	US-09-850-716A-341	Sequence 341, App
21	269	60.0	356	10	US-09-897-778-341	Sequence 341, App
22	191	42.6	586	10	US-09-735-705-152	Sequence 152, App
23	191	42.6	586	10	US-09-850-716A-152	Sequence 152, App
24	191	42.6	586	10	US-09-897-778-152	Sequence 152, App
25	22	4.9	635	12	US-10-155-059-3	Sequence 3, Appli
26	22	4.9	636	10	US-09-732-384-10	Sequence 10, Appl
27	9	2.0	71	9	US-10-007-557-9	Sequence 9, Appli
28	9	2.0	271	10	US-09-925-302-680	Sequence 680, App
29	9	2.0	293	10	US-09-968-958-2	Sequence 2, Appli
30	9	2.0	293	10	US-09-968-958-4	Sequence 4, Appli
31	9	2.0	319	9	US-09-968-851-42	Sequence 42, Appl
32	9	2.0	335	9	US-09-968-851-44	Sequence 44, Appl
33	9	2.0	353	9	US-09-968-851-40	Sequence 40, Appl
34	9	2.0	353	9	US-10-146-473-78	Sequence 78, Appl
35	9	2.0	363	9	US-09-968-851-26	Sequence 26, Appl
36	9	2.0	374	9	US-09-968-851-28	Sequence 28, Appl
37	9	2.0	381	9	US-09-968-851-36	Sequence 36, Appl
38	9	2.0	390	9	US-10-038-010-6	Sequence 6, Appli
39	9	2.0	393	9	US-09-029-327-4	Sequence 4, Appli
40	9	2.0	393	9	US-09-860-286-9	Sequence 9, Appli
41	9	2.0	393	10	US-09-776-695-32	Sequence 32, Appl
42	9	2.0	393	10	US-09-732-384-3	Sequence 3, Appli
43	9	2.0	393	10	US-09-860-211-9	Sequence 9, Appli
44	9	2.0	394	12	US-10-155-059-4	Sequence 4, Appli
45	9	2.0	401	9	US-09-968-851-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-735-705-340 Application US/09735705
; Sequence 340, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-735-705-340

Query Match	100.0%	Score 448;	DB 10;	Length 448;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MSQSTQTNFSLPEVFGHINDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60	
Qy	61	DSDSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTATSPYAQPSSTFDAL	120	
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QY 121 SPSPAIPTNDYPCPHSFDFVSFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPTNDYPCPHSFDFVSFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVCVMNRRLIIVTLETRDQGVLGRR 300
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVCVMNRRLIIVTLETRDQGVLGRR 300
QY 301 FEARICACPGDRKADESIRKQVSDSTKNGDKTKRFRQNTGHIQMTSIIKRRSPDDE 360
Db 301 FEARICACPGDRKADESIRKQVSDSTKNGDKTKRFRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420
QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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RESULT 2

US-09-850-716A-340
; Sequence 340, Application US/09850716A
; Patent No. US20020115139A1

GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850,716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 340

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-340

Query Match
Best Local Similarity 100.0%; Score 448; DB 10; Length 448;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DSLSLDPMPQYTNGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
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Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVCVMNRRLIIVTLETRDQGVLGRR 300
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Db 301 FEARICACPGDRKADESIRKQVSDSTKNGDKTKRFRQNTGHIQMTSIIKRRSPDDE 360

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Db 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 3

US-09-897-778-340

; Sequence 340, Application US/09897778

; Patent No. US20020147143A1

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 340

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-340

Query Match
Best Local Similarity 100.0%; Score 448; DB 10; Length 448;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSQSTQNEFLSPVFOHIDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
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Db 61 DSLSLDPMPQYTNGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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Db 121 SPSPAIPTNDYPCPHSFDFVSFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVCVMNRRLIIVTLETRDQGVLGRR 300
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Db 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420
QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
Db 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 4

US-09-735-705-344
; Sequence 344, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Banqur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344

Query Match 91.5%; Score 410; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSQSTQTNFELSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMD CIRMQ 60
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DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
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DB 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKKRRSPDDE 360
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QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQHLLQK 410
DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQHLLQK 410

RESULT 5

US-09-850-716A-344
; Sequence 344, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344

Query Match 91.5%; Score 410; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSQSTQTNFELSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMD CIRMQ 60
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRC 300
DB 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKKRRSPDDE 360
DB 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKKRRSPDDE 360
QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQHLLQK 410
DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQHLLQK 410

RESULT 6

US-09-897-778-344
; Sequence 344, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-344

Query Match 91.5%; Score 410; DB 10; Length 516;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Db	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Qy	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120
Db	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120
Qy	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Db	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Qy	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Db	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Qy	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Db	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Qy	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Db	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Qy	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410
Db	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410

RESULT 7

US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-339

Query Match 91.5%; Score 410; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Db	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Qy	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120
Db	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120

Qy	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Db	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Qy	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Db	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Qy	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Db	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Qy	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Db	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Qy	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410
Db	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410

RESULT 8

US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match 91.5%; Score 410; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Db	1	MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60
Qy	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120
Db	61	DSLDSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL	120
Qy	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Db	121	SPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP	180
Qy	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Db	181	POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP	240
Qy	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Db	241	ITGRQSVLPYEPVPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC	300
Qy	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Db	301	FEARICACPRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHGQIOMTSIKRRSPDDE	360
Qy	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410
Db	361	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIROOOOQHLLQK	410

```
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQOQQOHHLLQK 410

RESULT 9
US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Manerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 91.5%; Score 410; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 120
Db 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
QY 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300
Db 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300
QY 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360
Db 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQOQQOHHLLQK 410
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQOQQOHHLLQK 410

RESULT 10
US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
```

```
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 91.5%; Score 410; DB 10; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 40 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 120
Db 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 219
QY 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300
Db 280 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 339
QY 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360
Db 340 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 399
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQOQQOHHLLQK 410
Db 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQOQQOHHLLQK 449

RESULT 11
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342
```

Query Match 91.5%; Score 410; DB 10; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIWDFLEQICSVQPIDLNFVDEPSEGCATNKIEISMDICRMQ 60
DB 40 MSOSTOTNEFLSPEVFOHIWDFLEQICSVQPIDLNFVDEPSEGCATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDAL 120
DB 100 DSDLSDPMPQYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDAL 159
QY 121 SPSPAIPNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDP 279
QY 241 ITGRQSVLPVPEPPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 300
DB 280 ITGRQSVLPVPEPPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 339
QY 301 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
DB 340 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 399
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQK 410
DB 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQK 449

RESULT 12
US-09-897-778-342
; Sequence 342, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Warnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrik
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 91.5%; Score 410; DB 10; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIWDFLEQICSVQPIDLNFVDEPSEGCATNKIEISMDICRMQ 60
DB 40 MSOSTOTNEFLSPEVFOHIWDFLEQICSVQPIDLNFVDEPSEGCATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDAL 120
DB 100 DSDLSDPMPQYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDAL 159

QY 121 SPSPAIPNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDP 279
QY 241 ITGRQSVLPVPEPPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 300
DB 280 ITGRQSVLPVPEPPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 339
QY 301 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
DB 340 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 399
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQK 410
DB 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQK 449

RESULT 13
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lihun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-343

Query Match 76.1%; Score 341; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.9e-311;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 POYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPAPSN 129
DB 15 POYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPAPSN 74
QY 130 TDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTPPOGAVIRAM 189
DB 75 TDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTPPOGAVIRAM 134
QY 190 PVTAKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PVTAKAEHTEVVKRCPNHLSREFNEGOIAPPSSHILRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRCFEACAP 309
DB 195 PYEPQVGTETFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRCFEACAP 254
QY 310 GRORAKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDELLYLPVGR 369

Db 255 GRDRKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDELLYLPVGR 314

QY 370 ETYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHLLQK 410

Db 315 ETYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHLLQK 355

RESULT 14

US-09-850-716A-343

; Sequence 343, Application US/09850716A

; Patent No. US20020115139A1

; GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850,716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 343

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-343

Query Match 76.1%; Score 341; DB 10; Length 461;

Best Local Similarity 100.0%; Pred. No. 4.9e-311;

Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129

Db 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74

QY 130 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189

Db 75 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134

QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249

Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194

QY 250 PYEPPQVGTFTVLNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309

Db 195 PYEPPQVGTFTVLNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254

QY 310 GRDRKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDELLYLPVGR 369

Db 255 GRDRKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDELLYLPVGR 314

QY 370 ETYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHLLQK 410

Db 315 ETYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHLLQK 355

RESULT 15

US-09-897-778-343

; Sequence 343, Application US/09897778

; Patent No. US20020147143A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 343

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-343

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Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74

QY 130 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189

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QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249

Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194

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Search completed: June 24, 2003, 22:24:22

Job time : 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:58:28 ; Search time 3502 seconds

(without alignments)
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Gapop 60.0 , Capext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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9: gb_est1.*

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11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

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17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

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22: em_gss_fun.*

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25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	383	13.6	563	9	AL698768
4	383	13.6	563	9	AL698769
5	338	12.0	514	10	AW368378
6	335	11.9	657	10	AW368381

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c	8	317	11.3	637	10	AW368375	PM2-HT019
c	9	284	10.1	517	10	AW382125	CMO-HT032
c	10	275	9.8	498	9	AI809318	we96a04.x
c	11	257	9.1	293	10	BE145042	PM4-HT019
c	12	250	8.9	1177	13	BM455587	AGENCOURT
c	13	233	8.3	736	12	EG698692	602703045
c	14	230	8.2	565	10	AW379300	MRO-HT024
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c	17	213	7.6	480	12	BF083249	RC1-CY024
c	18	206	7.3	394	10	AW382679	PMO-HT033
c	19	201	7.1	421	12	BE706690	PMO-HT033
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ALIGNMENTS

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ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 1042)			
TITLE	NIH-MGC http://mgs.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Lou Staudt CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: Agencourt Bioscience Corporation found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM12268 row: d column: 20 High quality sequence stop: 660. Location/Qualifiers 1. .1042			


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SOURCE        human.
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AUTHORS        1 (bases 1 to 563)
TITLE          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL        EST (Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.)
COMMENT        Unpublished (1999)
CONTACT        Wambutt R
MIPS           Am Klopferspitz 18a D-82152 Martinsried, Germany
               This is the 5' sequence of the clone insert
               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
               Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
               sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
               consortium of the German Genome Project.
               No sl sequence available.
               This clone (DKFZp686H1410) is available at the RZPD in Berlin.
               Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
               Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES       source
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Db 421 GTCGGCCACCTGGAGCTATTCCACTGAAGTGAAGAACTCTACTGCCAAATTCGAAGAC 480
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Best Local Similarity 100.0%; Pred. No. 4e-178;
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LOCUS
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VERSION        AL698769.1  GI:19619309
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SOURCE        human.
ORGANISM      Homo sapiens
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AUTHORS        1 (bases 1 to 563)
TITLE          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL        EST (Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.)
COMMENT        Unpublished (1999)
CONTACT        Wambutt R
MIPS           Am Klopferspitz 18a D-82152 Martinsried, Germany
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               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
               Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
               sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
               consortium of the German Genome Project.
               No sl sequence available.
               This clone (DKFZp686H1810) is available at the RZPD in Berlin.
               Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
               Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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BASE COUNT    152 a 175 c 128 g 108 t
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Query Match      13.6%; Score 383; DB 9; Length 563;
Best Local Similarity 100.0%; Pred. No. 4e-178;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 351 GCCACAGTACAGAACCTGGGGCTCTGACAGCATGGACGAGATTCAGAACGGCTC 410
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Qy 651 ATGCCCATCCAGATCAAGTGTGATGACCCACCTCTCTCAGGAGCTGTATTCCGGCCAT 710
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RESULT 5
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AW368378
LOCUS
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VERSION AW368378.1 GI:6873028
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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/dev_stage="Adult"
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 139 a 150 c 155 g 192 t
ORIGIN
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Best Local Similarity 99.5%; Pred. No. 7.4e-154;
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DEFINITION PM2-HT0190-081099-001-a07 HT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW368375
VERSION AW368375.1 GI:6873025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&td=PM2-HT0190-
081099-001-a07&t3=1999-10-08&t4=1)
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High quality sequence start: 14
High quality sequence stop: 589.
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Location/Qualifiers
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 136 a 146 c 161 g 194 t
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Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

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DB 101 GAGATGGCAAGTCCTGGCGGACGCTGCTTTGAGCGCCGATCTGTGCTTGGCCAGAA 160
QY 1076 GAGACAGGAGCGCGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAGA 1135
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ACCESSION  AW379296
VERSION    AW379296.1 GI:6883955
KEYWORDS   EST.
SOURCE     human.
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REFERENCE  1 (bases 1 to 508)
            HGCP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
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                    Site 2: SmaI; A mini-library was made by cloning products
                    derived from ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
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Best Local Similarity 100.0%; Pred. No. 7.2e-99;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 278 CATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCGCAGATGATGAAGTGTATATAC 337
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SUMMARIES

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9	1296	46.0	1347	20	AAZ58574 Human cell regulat

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11	1275	45.3	4849	21	AAC66031 Human lung cancer-
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17	1141	40.5	1182	20	AAZ58576 Human cell regulat
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19	1026	36.4	1386	24	ABL49251 Human cell regulat
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ALIGNMENTS

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DT Human p51 encoding cDNA A.
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KW tumour suppression; diagnosis; ss.
XX Homo sapiens.
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XX WO9950412-A1.
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XX PD 07-OCT-1999.
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XX PF 24-MAR-1999; 99WO-JP01512.
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XX PR 27-MAR-1998; 98JP-0100467.
XX
XX PA (SAKA) OTSUKA PHARM CO LTD.
XX (IKAW/) IKAWA Y.

PI	Ikawa Y, Ikawa S, Obinata M;	
XX	WPI; 1999-591318/50.	
DR	P-PSDB; AAY45246.	
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PT	treatment of cancers and screening for potential cell proliferation	
PT	agents -	
XX		
PS	Claim 3; Page 148-151; 163pp; Japanese.	
XX		
CC	The present sequence represents a human p51 gene, which is related to	
CC	p53 and has cell proliferation regulation and tumour suppression	
CC	activity. The p51 gene can be used in the investigation, diagnosis and	
CC	treatment of diseases such as cancer, with which the p53 family cell	
CC	proliferation regulation is associated. The p51 protein may be used for	
CC	screening potential agonists and antagonists of its regulatory function,	
CC	for use as drugs,	
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2461 CTGATACTGTTCACTGATTTAGCCAGGAGACTTTACGTTTGTAGTAAGTGAGATCCAGC 2520
2521 AGACGTGTTAAATCAGCAGCTCCCTGGACTGGAAATTAAGATTTGAAGGGGTAGACTATT 2580
2521 AGACGTGTTAAATCAGCAGCTCCCTGGACTGGAAATTAAGATTTGAAGGGGTAGACTATT 2580
2581 TTCTTTTCTTACCAAAAGTTTAGAATCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2640
2581 TTCTTTTCTTACCAAAAGTTTAGAATCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2640
2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTCTCCCTCCCTCAATCTTCCACACCCAGT 2700
2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTCTCCCTCCCTCAATCTTCCACACCCAGT 2700
2701 CACCAGCAGCTGATTTCTGTCCCAAGACAAATGATTTCTTGTATTGAGGCTGTGCTT 2760
2701 CACCAGCAGCTGATTTCTGTCCCAAGACAAATGATTTCTTGTATTGAGGCTGTGCTT 2760
2761 TTGTGGATGTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2816
2761 TTGTGGATGTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2816

RESULT 2
AAC66029 standard; cDNA; 2816 BP.
XX
AC AAC66029;

XX 21-FEB-2001 (first entry)
DT Human lung cancer-associated cDNA p63 isoform 3.
DE Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection; ss.
XX Homo sapiens.
OS
FN WO2000061612-A2.
PD 19-OCT-2000.
PF 03-APR-2000; 2000WO-US08896.
XX 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
FA
XX Wang T, Fan L;
PI WPI: 2000-628399/60.
XX P-PSDB; AAB11359.
DR
DR
XX
PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
PS Claim 25a; Page 238-239; 261pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
SQ Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;

Query Match 100.0%; Score 2816; DB 21; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTTGATATCAAAAGACAGAGTTGAAGGAATGAATTTGAAACTTACCGTGTGCCACCT 60
DB 1 TCGTTGATATCAAAAGACAGAGTTGAAGGAATGAATTTGAAACTTACCGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCTTGTGTAGAAAACCCAGCTTCCTCTGG 120
DB 61 ACAGTACTGCCCTGACCCCTTACATCCAGCTTGTGTAGAAAACCCAGCTTCCTCTGG 120
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCCTAGAGACACACAGAAATGAATTCCTCAGT 180
DB 121 AAAGAAAGTTATTACCGATCCACCATGTCCTAGAGACACACAGAAATGAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCCTATATGTTTCAGTTCAGCCC 240
DB 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCCTATATGTTTCAGTTCAGCCC 240
QY 241 ATTGACTTGAACCTTTGTGGATGAACCATCATCAGAAGATGTTGGACAAACAAAGTTCAGATT 300
DB 241 ATTGACTTGAACCTTTGTGGATGAACCATCATCAGAAGATGTTGGACAAACAAAGTTCAGATT 300

QY	301	AGCATGGACTGTATCCGATGCGAGCTCGGACCTGAGTGAACCCCATCTGTGGCCACAGTAC	360		1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAATCT	1440
Db	301	AGCATGGACTGTATCCGATGCGAGCTCGGACCTGAGTGAACCCCATCTGTGGCCACAGTAC	360				
QY	361	ACGAACCTGGGGCTCTTGAACAGCATGACAGCATGATTCAGAACGGCTCCTGGTCCACC	420		1441	GAGCTCTTCTTTAGACATTCCAAAGCCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC	1500
Db	361	ACGAACCTGGGGCTCTTGAACAGCATGACAGCATGATTCAGAACGGCTCCTGGTCCACC	420		1441	GAGCTCTTCTTTAGACATTCCAAAGCCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC	1500
QY	421	AGTCCCTATTAACACAGACACCGGCGAGAACAGGGTACAGGGCGCCCTCGCCCTACGCACAG	480		1501	TCATATTTTAAAGTGTGTGTGTATTTCCATGTCTATATGTGAGTGTGTGTGTGTGTA	1560
Db	421	AGTCCCTATTAACACAGACACCGGCGAGAACAGGGTACAGGGCGCCCTCGCCCTACGCACAG	480		1501	TCATATTTTAAAGTGTGTGTGTATTTCCATGTCTATATGTGAGTGTGTGTGTGTA	1560
QY	481	CCAGACTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACACCGACTAC	540		1561	TGTGTGCGTGTGTATCTAGCCCTCATAAACAGAGACTTCAAGACACTTTGGCTCAGAGA	1620
Db	481	CCAGACTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACACCGACTAC	540		1561	TGTGTGCGTGTGTATCTAGCCCTCATAAACAGAGACTTCAAGACACTTTGGCTCAGAGA	1620
QY	541	CCAGGCCCGCACAGTTTCGACGTGCTCTCCAGCAGTCGAGACCGCCAGTGGCCACC	600		1621	CCCAACTGCTCAAAAGCCACAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACT	1680
Db	541	CCAGGCCCGCACAGTTTCGACGTGCTCTCCAGCAGTCGAGACCGCCAGTGGCCACC	600		1621	CCCAACTGCTCAAAAGCCACAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACT	1680
QY	601	TGGACGTATTCCTACTGAAGAACTCTACTGCGCAATTCGAAGACATGCCCATC	660		1681	TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCTTACCGGCCATTGGTGGGTGAG	1740
Db	601	TGGACGTATTCCTACTGAAGAACTCTACTGCGCAATTCGAAGACATGCCCATC	660		1681	TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCTTACCGGCCATTGGTGGGTGAG	1740
QY	661	CAGATCAAGTGTATGACCCACCTCCTCAGGGAGCTGTATCCGCGCCATGCCGTCTAC	720		1741	GAACCACTGTGTTGCTGTGAGCTTCTGTTGTTCTCTGGAGGGAGGGTCAAGTGGG	1800
Db	661	CAGATCAAGTGTATGACCCACCTCCTCAGGGAGCTGTATCCGCGCCATGCCGTCTAC	720		1741	GAACCACTGTGTTGCTGTGAGCTTCTGTTGTTCTCTGGAGGGAGGGTCAAGTGGG	1800
QY	721	AAAAAGCTGAGCAGCTCAGGAGGTGGTGAACGGTGGCCCAACCATGAGCTGAGCGT	780		1801	GAAAGGGGATTAAGATGTTTATGGAACCCCTTCTGCTCTCTCTGTTCTTCTTCTTAA	1860
Db	721	AAAAAGCTGAGCAGCTCAGGAGGTGGTGAACGGTGGCCCAACCATGAGCTGAGCGT	780		1801	GAAAGGGGATTAAGATGTTTATGGAACCCCTTCTGCTCTCTCTGTTCTTCTTCTTAA	1860
QY	781	GAATTCACGAGGACAGATGGCCCTCCTAGTCAATTTGATTCGAGTAGGGGAACAGC	840		1861	AATTCACAGGAGCTTTTGGACAGCTCTCAAACTTAAGATGCTTTTTTAAAGAAAGAG	1920
Db	781	GAATTCACGAGGACAGATGGCCCTCCTAGTCAATTTGATTCGAGTAGGGGAACAGC	840		1861	AATTCACAGGAGCTTTTGGACAGCTCTCAAACTTAAGATGCTTTTTTAAAGAAAGAG	1920
QY	841	CATGCCAGTATGTAGAAGATCCATCAGAGGAGACAGTGTGCTGCTTATGAG	900		1921	AAAAAGTTGTTATTTGCTGTGCATTAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT	1980
Db	841	CATGCCAGTATGTAGAAGATCCATCAGAGGAGACAGTGTGCTGCTTATGAG	900		1921	AAAAAGTTGTTATTTGCTGTGCATTAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT	1980
QY	901	CCACCCAGGTTGGCAGTGAATTCAGCAGTCTTGTACAAATTCATGTTAAGACAGT	960		1981	CCCTTTTAAATGCTGCTCATGTAATATTGCAAGTGTAGTGTAGTGTAGTGTAGTGT	2040
Db	901	CCACCCAGGTTGGCAGTGAATTCAGCAGTCTTGTACAAATTCATGTTAAGACAGT	960		1981	CCCTTTTAAATGCTGCTCATGTAATATTGCAAGTGTAGTGTAGTGTAGTGTAGTGT	2040
QY	961	TGTGTTGGAGGATGAACCGCTCCAAATTTAATCATTTGTTACTGTGAAACAGAGAT	1020		2041	TACTGCTGGCAGCAGGTGATCATTAACAAAAGTAACTAATTTGTTGGTGGAGAGTTC	2100
Db	961	TGTGTTGGAGGATGAACCGCTCCAAATTTAATCATTTGTTACTGTGAAACAGAGAT	1020		2041	TACTGCTGGCAGCAGGTGATCATTAACAAAAGTAACTAATTTGTTGGTGGAGAGTTC	2100
QY	1021	GGCAAGTCTTGGCCGACGCTGTTTGGGCGCGGATCTGTGCTTGGCCAGGAGAGAC	1080		2101	TTTGTGAGAACTTGCTATTTGCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGTGT	2160
Db	1021	GGCAAGTCTTGGCCGACGCTGTTTGGGCGCGGATCTGTGCTTGGCCAGGAGAGAC	1080		2101	TTTGTGAGAACTTGCTATTTGCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGTGT	2160
QY	1081	AGGAAGCGGATGAAGATAGCATGAGAAAGCAGAGTTTCGACAGTACAAAGACGCT	1140		2161	GCTGTACCTGCTCTGCCACTGTATGTTGGCATCTGTATGCTTAAAGTTTTTCTGTGTA	2220
Db	1081	AGGAAGCGGATGAAGATAGCATGAGAAAGCAGAGTTTCGACAGTACAAAGACGCT	1140		2161	GCTGTACCTGCTCTGCCACTGTATGTTGGCATCTGTATGCTTAAAGTTTTTCTGTGTA	2220
QY	1141	GATGTGACGAGCGGCTTTCGTGAGAACACACATGATGATGATGATGATGATGATGAT	1200		2221	CATGAAACCCCTGGAGAGCCTACTACAAAAGTCTGTTGGCCCCCATAGCAGGTGAA	2280
Db	1141	GATGTGACGAGCGGCTTTCGTGAGAACACACATGATGATGATGATGATGATGATGAT	1200		2221	CATGAAACCCCTGGAGAGCCTACTACAAAAGTCTGTTGGCCCCCATAGCAGGTGAA	2280
QY	1201	AAACGAAGATCCCGATGATGAATGTTATATCTTACCAGTGGGGCGGTGAGACTTAT	1260		2281	CTCATTTTGTGCTTTTAAATAGAACACAAATCCACCCAGTAATATGCCCTTAGGTAGT	2340
Db	1201	AAACGAAGATCCCGATGATGAATGTTATATCTTACCAGTGGGGCGGTGAGACTTAT	1260		2281	CTCATTTTGTGCTTTTAAATAGAACACAAATCCACCCAGTAATATGCCCTTAGGTAGT	2340
QY	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCACTCTCCCTCAGCACACA	1320		2341	TGTTTACCATTTTCAAAAGCTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGAT	2400
Db	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCACTCTCCCTCAGCACACA	1320		2341	TGTTTACCATTTTCAAAAGCTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGAT	2400
QY	1321	ATTGAAACCTACAGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380		2401	AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTTACCTACCAATAAAACACGACCATATTA	2460
Db	1321	ATTGAAACCTACAGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380		2401	AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTTACCTACCAATAAAACACGACCATATTA	2460
QY	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAATCT	1440		2461	CTGATACTGTTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT	2520

Db 2461 CTGATACGTGTTCACTGTCATTTAGCCAGAGACTTTACGTTTTAGTAAGTGAAGTCCCAAGC 2520
Qy 2521 AGACGTGTTAAATCAGACACTCCCTGGAGTGAATTAAGATTGAAAGGGTAGACTACTT 2580
Db 2521 AGACGTGTTAAATCAGACACTCCCTGGAGTGAATTAAGATTGAAAGGGTAGACTACTT 2580
Qy 2581 TTTCTTTTTTACCAAAAGTTTAGAGAATCTCTGTTTCTTTCATTTTAAACATATT 2640
Db 2581 TTTCTTTTTTACCAAAAGTTTAGAGAATCTCTGTTTCTTTCATTTTAAACATATT 2640
Qy 2641 TTAAGATAATAGCATAAGACTTTAAAGATGTTTCCCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATAATAGCATAAGACTTTAAAGATGTTTCCCTCCCTCCATCTTCCACACCCAGT 2700
Qy 2701 CACCAGCAGCTGATTTCTGTGCACCAAGACAAATCATTTCTGTTTATGAGGCTGTGCTT 2760
Db 2701 CACCAGCAGCTGATTTCTGTGCACCAAGACAAATCATTTCTGTTTATGAGGCTGTGCTT 2760
Qy 2761 TTGTGGATGTGATTTTAAATTTCAATAAATTTTGCATCTTGGTTTAAAGAAA 2816
Db 2761 TTGTGGATGTGATTTTAAATTTCAATAAATTTTGCATCTTGGTTTAAAGAAA 2816

RESULT 3

AAF86588
ID AAF86588 standard; DNA; 2816 BP.

XX AC AAF86588;

XX DT 03-AUG-2001 (first entry)

XX DE Human gene #1 used to produce a chimeric p53 gene.

XX KW Human; cytostatic; gene therapy; p53; human tumour; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers
FH 145..1491
CDS /*tag= a

FT /*product= "Human protein"

FT 2786..2791

FT /*tag= b

XX JP2000354488-A.

XX PD 26-DEC-2000.

XX PF 09-APR-1999; 99JP-0139034.

XX PR 09-APR-1999; 99JP-0139034.

XX PA (IKAW/) IKAWA H.

XX PA (SAKA) OTSUKA PHARM CO LTD.

XX WIPI; 2001-268293/28.

XX P-PSDB; AAB82128.

PT Chimera gene of the p53 family, useful for gene therapy, and treatment
PT of cancer, comprises a transcription activating region and a DNA
PT binding region -

XX PS Example 1; Page 32-36; 57pp; Japanese.

XX CC The present invention relates to a chimera gene of p53 family encoding a
CC transcription activating region, a DNA binding region, and an oligomer
CC formation region of different p53 family proteins. The chimera gene can
CC be used for gene therapy of p53 variant human tumours, and analysis of
CC the function of the p53 family gene. The present sequence was used in the
CC present invention.

XX SQ Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;

Query Match 100.0%; Score 2816; DB 22; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAATTTTGAATCTTCCACGGTGTGCCACCCCT 60
Db 1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAATTTTGAATCTTCCACGGTGTGCCACCCCT 60
Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCTGTAGAAAACCCAGCTCATTTCTCTTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCTGTAGAAAACCCAGCTCATTTCTCTTGG 120
Qy 121 AAAGAAAGTTATTACCGATCCACCATGTCACAGAGACACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCACAGAGACACAGACAAATGAATTCCTCAGT 180
Qy 181 CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTTCAGTTTCCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTTCAGTTTCCAGCCC 240
Qy 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGATGTTGCGACAACAAGATTGAGATT 300
Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGATGTTGCGACAACAAGATTGAGATT 300
Qy 301 AGCATGGACTGTATCCGCATGCGAGACTCGGACCTGAGTGCACCCCATGTGGCCACAGTAC 360
Db 301 AGCATGGACTGTATCCGCATGCGAGACTCGGACCTGAGTGCACCCCATGTGGCCACAGTAC 360
Qy 361 ACAGACCTGGGGCTCTCTGAACAGCATGACAGCATGATTCAGAGCGGTCTCTGTCACACC 420
Db 361 ACAGACCTGGGGCTCTCTGAACAGCATGACAGCATGATTCAGAGCGGTCTCTGTCACACC 420
Qy 421 AGTCCTATACAGACACGCGCAGAACAGCGTCACGGCGCCCTGCCCTTACGACACAG 480
Db 421 AGTCCTATACAGACACGCGCAGAACAGCGTCACGGCGCCCTGCCCTTACGACACAG 480
Qy 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTTCAACACACCAGTAC 540
Db 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTTCAACACACCAGTAC 540
Qy 541 CCAGCGCGCACAGTTTCGACGTGCTTCCAGCAGTGCAGCAGCGCCCAAGTGGCCACC 600
Db 541 CCAGCGCGCACAGTTTCGACGTGCTTCCAGCAGTGCAGCAGCGCCCAAGTGGCCACC 600
Qy 601 TGGAGCTATTCACCTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
Db 601 TGGAGCTATTCACCTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
Qy 661 CAGATCAAGTGTAGTACCCCTCCTCAGGGAGCTGTTATCCGGCCCATGCCTGTCTAC 720
Db 661 CAGATCAAGTGTAGTACCCCTCCTCAGGGAGCTGTTATCCGGCCCATGCCTGTCTAC 720
Qy 721 AAAAAGCTGAGCAGCTCAGGAGTGTGAAGGGTGCCTCCCAACCATGAGTGAAGCGT 780
Db 721 AAAAAGCTGAGCAGCTCAGGAGTGTGAAGGGTGCCTCCCAACCATGAGTGAAGCGT 780
Qy 781 GAATTCACGAGGACAGATTGCCCTCCTCTAGTCTATTTGATTTCGAGTAGAGGGGAACAGC 840
Db 781 GAATTCACGAGGACAGATTGCCCTCCTCTAGTCTATTTGATTTCGAGTAGAGGGGAACAGC 840
Qy 841 CATCCCCAGTATGAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGTATGAG 900
Db 841 CATCCCCAGTATGAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGTATGAG 900
Qy 901 CCACCCAGGTTGGCACTGAATTCAGGACAGTCTTGTACAATTTTCATGTTAAGCAGT 960
Db 901 CCACCCAGGTTGGCACTGAATTCAGGACAGTCTTGTACAATTTTCATGTTAAGCAGT 960
Qy 961 TGTGTGGAGGATGAACCCCGTCCCAATTTTAAATCATTTGTTACTTCTGGAACACAGAT 1020
Db 961 TGTGTGGAGGATGAACCCCGTCCCAATTTTAAATCATTTGTTACTTCTGGAACACAGAT 1020
Qy 1021 GGGCAAGTCTTGGGCCGACGCTGCTTTGAGGCCCGGATCTGCTGTTGCCAGGAGAGAC 1080

[illegible]

Db	2101	TTTGTGAGAACTTGCAATTAATTTGTGCTCCTCCCTCATGTGTAGTAGCAACATTTCTTAAT	2116
QY	2161	GCTGTGTACTCGCTCGCCACTGTATGTTGGCAATCTGTTATGCTAAAGTTTTTCTTGTA	2220
Db	2161	GCTGTGTACTCGCTCGCCACTGTATGTTGGCAATCTGTTATGCTAAAGTTTTTCTTGTA	2220
QY	2221	CATGAACCCCTGGAGAGCCTACTACAAAAAAGCTGTTGTTGGGCCCCCATAGCAGGTGAA	2280
Db	2221	CATGAACCCCTGGAGAGCCTACTACAAAAAAGCTGTTGTTGGGCCCCCATAGCAGGTGAA	2280
QY	2281	CTCATTTTGTGCTTTTAATAGAAAGACAATCCACCCAGTAATATTGGCCCTTACGTAGT	2340
Db	2281	CTCATTTTGTGCTTTTAATAGAAAGACAATCCACCCAGTAATATTGGCCCTTACGTAGT	2340
QY	2341	TGTTTTACCATTATTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT	2400
Db	2341	TGTTTTACCATTATTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT	2400
QY	2401	AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATATAAACCCAGCATATTA	2460
Db	2401	AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATATAAACCCAGCATATTA	2460
QY	2461	CTGATACCTGTTTCAGTGCATTTTAGCCAGGAGACTTACGTTTTTGTAGTAAGTCAGATCCAAGC	2520
Db	2461	CTGATACCTGTTTCAGTGCATTTTAGCCAGGAGACTTACGTTTTTGTAGTAAGTCAGATCCAAGC	2520
QY	2521	AGACGTGTTAAATCAGACCTCTCGACTCGAAATTAAGATTGAAAGGTAGACTACTTT	2580
Db	2521	AGACGTGTTAAATCAGACCTCTCGACTCGAAATTAAGATTGAAAGGTAGACTACTTT	2580
QY	2581	TTCCTTTTTTTTACTCAAAAGTTTAGAATCTCTGTTCTTCCATTTTAAAAACATATT	2640
Db	2581	TTCCTTTTTTTTACTCAAAAGTTTAGAATCTCTGTTCTTCCATTTTAAAAACATATT	2640
QY	2641	TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCCTCCATCTCCACACCCAGT	2700
Db	2641	TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCCTCCATCTCCACACCCAGT	2700
QY	2701	CACACAGACTGATTTTCTGTCCACAGACAATGATTTCTGTTATTGAGGCTGTGCTT	2760
Db	2701	CACACAGACTGATTTTCTGTCCACAGACAATGATTTCTGTTATTGAGGCTGTGCTT	2760
QY	2761	TTTGGGATGTGATTTTAATTTTCAATAAAGCTTTTGGCATCTGCTTTAAAGAAA	2816
Db	2761	TTTGGGATGTGATTTTAATTTTCAATAAAGCTTTTGGCATCTGCTTTAAAGAAA	2816
RESULT 4			
ABLA9248			
ID	ABLA9248 standard; cdna; 2816 bp.		
XX			
AC	ABLA9248;		
XX			
DT	01-MAY-2002 (first entry)		
XX			
DE	Human p53 homologue isoform, p63 (L530S) cdna sequence SEQ ID NO:333.		
XX			
KW	Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;		
XX	immune response; ss.		
OS	Homo sapiens.		
XX			
FN	WO200200174-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	28-JUN-2001; 2001WO-US21065.		
XX			
PR	28-JUN-2000; 2000US-0606421.		
XX			
PR	02-AUG-2000; 2000US-0630940.		
XX			
PR	21-AUG-2000; 2000US-0643597.		
XX			
PR	15-SEP-2000; 2000US-0662786.		
XX			
PR	09-OCT-2000; 2000US-0685696.		

Db 121 AAGAAAGTTATTACCGATCCACCATTGCCAGACACACAAATGAATTCCTCAGT 180
Qy 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGACACAGCCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGACACAGCCTATATGTTTCAGTTCAGCCC 240
Qy 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGTGGACAAACAAAGATTGAGATT 300
Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGTGGACAAACAAAGATTGAGATT 300
Qy 301 AGCATGGAGTGTATCCGATCGAGACTCGAGACTCGAGACTGAGTCCAGTGGCCACAGTAC 360
Db 301 AGCATGGAGTGTATCCGATCGAGACTCGAGACTCGAGACTGAGTCCAGTGGCCACAGTAC 360
Qy 361 AGCAACCTGGGGCTCTCTGAACAGATGGACAGCAGATTTCAGAACGGCTCTCTGTCACCC 420
Db 361 AGCAACCTGGGGCTCTCTGAACAGATGGACAGCAGATTTCAGAACGGCTCTCTGTCACCC 420
Qy 421 AGTCCCTATAACAGACACCGCGGAGAACAGCTCAGCGGCGCTCGCCCTACGCACAG 480
Db 421 AGTCCCTATAACAGACACCGCGGAGAACAGCTCAGCGGCGCTCGCCCTACGCACAG 480
Qy 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCTCCACACCGAGTAC 540
Db 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCTCCACACCGAGTAC 540
Qy 541 CCAGGCGGACAGTTCGAGGCTCTCTCCAGCAGTCGACACCGCCAAAGTGGGCCACC 600
Db 541 CCAGGCGGACAGTTCGAGGCTCTCTCCAGCAGTCGACACCGCCAAAGTGGGCCACC 600
Qy 601 TGGAGCTATTCACCTGAACCTGAGGAGCTGTTATCGCGGCGCATCGCTGCTAC 720
Db 601 TGGAGCTATTCACCTGAACCTGAGGAGCTGTTATCGCGGCGCATCGCTGCTAC 720
Qy 721 AAAAAAGCTGAGCAGCTGAGGAGTGGTGAAGCGGTGCGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAAGCTGAGCAGCTGAGGAGTGGTGAAGCGGTGCGCCCAACCATGAGCTGAGCCGT 780
Qy 781 GAATTCACAGGAGGACAGATTGCCCTCTCTAGTTCATTGATTCGAGTAGAGGGAACAGC 840
Db 781 GAATTCACAGGAGGACAGATTGCCCTCTCTAGTTCATTGATTCGAGTAGAGGGAACAGC 840
Qy 841 CATGCCAGTATGAGAGATCCATCAGAGGAGCAGAGTGTGCTGCTGATGAG 900
Db 841 CATGCCAGTATGAGAGATCCATCAGAGGAGCAGAGTGTGCTGCTGATGAG 900
Qy 901 CCACCCAGGTTGGCAGTGAATTCAGCAGAGTCTTGTACAAATTCATGTTGTAACAGCAGT 960
Db 901 CCACCCAGGTTGGCAGTGAATTCAGCAGAGTCTTGTACAAATTCATGTTGTAACAGCAGT 960
Qy 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAACACAGAGAT 1020
Db 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAACACAGAGAT 1020
Qy 1021 GGCAAGTCTTGGCGGAGCTGCTTTGAGCGCGGATGCTGCTGCCAGGAGAGAC 1080
Db 1021 GGCAAGTCTTGGCGGAGCTGCTTTGAGCGCGGATGCTGCTGCCAGGAGAGAC 1080
Qy 1081 AGGAAGCGGATGAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGT 1140
Db 1081 AGGAAGCGGATGAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGT 1140
Qy 1141 GATGTTACCAAGCGCGGTTTCGTCAGACACAGATGTTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGTTACCAAGCGCGGTTTCGTCAGACACAGATGTTATCCAGATGACATCCATCAAG 1200
Qy 1201 AAACGAAGATCCCGAGATGATGAATGTTATCTTACCAGTGAAGGCGCGTGAGACTTAT 1260
Db 1201 AAACGAAGATCCCGAGATGATGAATGTTATCTTACCAGTGAAGGCGCGTGAGACTTAT 1260

Qy 1261 GAAATGCTGTGAAGATCAAGAGTCCCTCGAATCATGTAGTACCTTCTCTCAGCACACA 1320
Db 1261 GAAATGCTGTGAAGATCAAGAGTCCCTCGAATCATGTAGTACCTTCTCTCAGCACACA 1320
Qy 1321 ATTCAAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376
Db 1321 ATTCAAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376

RESULT 7

AAF86589

ID AAF86589 standard; DNA; 2270 BP.

XX AAF86589;

AC AAF86589;

XX 03-AUG-2001 (first entry)

XX Human gene #2 used to produce a chimeric p53 gene.

XX Human; cytostatic; gene therapy; p53; human tumour; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 145..2070

XX FT /*tag= a

XX FT /product= "Human protein"

XX PN JP2000354488-A.

XX XX 26-DEC-2000.

XX PF 09-APR-1999; 99JP-0139034.

XX XX 09-APR-1999; 99JP-0139034.

XX PR (IKAW/) IKAWA H.

XX PA (SAKA) OTSUKA PHARM CO LTD.

XX XX WPI: 2001-268293/28.

XX DR P-PSDB; AAB82129.

XX XX Chimera gene of the p53 family, useful for gene therapy, and treatment

XX PT of cancer, comprises a transcription activating region and a DNA

XX PT binding region

XX PS Example 1; Page 40-44; 57pp; Japanese.

XX CC The present invention relates to a chimera gene of p53 family encoding a

XX CC transcription activating region, a DNA binding region, and an oligomer

XX CC formation region of different p53 family proteins. The chimeric gene can

XX CC be used for gene therapy of p53 variant human tumours, and analysis of

XX CC the function of the p53 family gene. The present sequence was used in the

XX CC present invention.

XX SQ Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;

XX Query Match 48.9%; Score 1376; DB 22; Length 2270;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 TCGTTGATATCAAGACAGTTCAGGAAATGAATTTGAAACTTCACGGTGTGCCACCT 60

XX Db 1 TCGTTGATATCAAGACAGTTCAGGAAATGAATTTGAAACTTCACGGTGTGCCACCT 60

XX Qy 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120

XX Db 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120

XX Qy 121 AAGAAAGTTATTATCCGATCCACCATGTCCAGAGCACACAGAAATGAATTCCTCAGT 180

XX Db 121 AAGAAAGTTATTATCCGATCCACCATGTCCAGAGCACACAGAAATGAATTCCTCAGT 180

	Db		61	ACAGTACTGCCCTGACCCCTTAGCATCAGCGTTTCGTAGAAACCAGCTCATTTCTCTTG	120
	QY		121	AAAGAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAATAAATTCCTCAGT	180
	Db		121	AAAGAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAATAAATTCCTCAGT	180
	QY		181	CCAGAGTTTTCCAGCATATCTGGGATTTCTTGGGAACAGCCTATATGTTCAAGTTCAGGCC	240
	Db		181	CCAGAGTTTTCCAGCATATCTGGGATTTCTTGGGAACAGCCTATATGTTCAAGTTCAGGCC	240
	QY		241	ATTGACTTGAACCTTTGGATGAACCATCAGAAAGATGTGGACAAAACAAGATTCAGATT	300
	Db		241	ATTGACTTGAACCTTTGGATGAACCATCAGAAAGATGTGGACAAAACAAGATTCAGATT	300
	QY		301	AGCATGGACTGTATCCGATCGAGGACTCGGACCTTGAGTGAACCCCATGTGGCCACAGTAC	360
	Db		301	AGCATGGACTGTATCCGATCGAGGACTCGGACCTTGAGTGAACCCCATGTGGCCACAGTAC	360
	QY		361	ACGAACCTGGGGCTCCTGAACAGCATGACACGAGATTCAGAACGGCTCTCGTCCACC	420
	Db		361	ACGAACCTGGGGCTCCTGAACAGCATGACACGAGATTCAGAACGGCTCTCGTCCACC	420
	QY		421	AGTCCCTATACACAGACCCAGCGGAGAACCGCTCAGCGGCCTCGCCCTAGCCACAG	480
	Db		421	AGTCCCTATACACAGACCCAGCGGAGAACCGCTCAGCGGCCTCGCCCTAGCCACAG	480
	QY		481	CCAGCTCCACTTCGATGCTCTCTCCCATCACCGGCATCCCTCCAACACCGACTAC	540
	Db		481	CCAGCTCCACTTCGATGCTCTCTCCCATCACCGGCATCCCTCCAACACCGACTAC	540
	QY		541	CCAGGCCGACAGTTTGAGCGTTCCTCCAGCAGTCGAGCACCGCCAAAGTCGGCCACC	600
	Db		541	CCAGGCCGACAGTTTGAGCGTTCCTCCAGCAGTCGAGCACCGCCAAAGTCGGCCACC	600
	QY		601	TGGACGTATTCCACTGAACTGAAGAACTCTACTGCCAAATGCGAAAGACATGCCCATC	660
	Db		601	TGGACGTATTCCACTGAACTGAAGAACTCTACTGCCAAATGCGAAAGACATGCCCATC	660
	QY		661	CAGATCAAGGTGATGACCCCACTCTCCAGGAGCTGTATTCGGCGCATCGCTGTCTAC	720
	Db		661	CAGATCAAGGTGATGACCCCACTCTCCAGGAGCTGTATTCGGCGCATCGCTGTCTAC	720
	QY		721	AAAAAGCTGAGCAGCTCAGGAGGTGTTCAAGCGGTGCCCAAACCATGAGCTGAGCCGT	780
	Db		721	AAAAAGCTGAGCAGCTCAGGAGGTGTTCAAGCGGTGCCCAAACCATGAGCTGAGCCGT	780
	QY		781	GAAFTCAACGAGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC	840
	Db		781	GAAFTCAACGAGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC	840
	QY		841	CATGCCCAATGATAGNAGATCCCATCAGGAAGACAGATGTGCTGGTACCTTATGAG	900
	Db		841	CATGCCCAATGATAGNAGATCCCATCAGGAAGACAGATGTGCTGGTACCTTATGAG	900
	QY		901	CCACCCAGGTTGGCACTGAATTCAGCAGACTCTGTACAATTTCAATGTTACAGTACAGCAST	960
	Db		901	CCACCCAGGTTGGCACTGAATTCAGCAGACTCTGTACAATTTCAATGTTACAGTACAGCAST	960
	QY		961	TGTGTTGGAGGGATGAACCCCGTCCAAATTTTAATCATTTGTTACTCTGGAACACAGAGAT	1020
	Db		961	TGTGTTGGAGGGATGAACCCCGTCCAAATTTTAATCATTTGTTACTCTGGAACACAGAGAT	1020
	QY		1021	GGCAAGTCTTGGGCGACGCTGTTTGGAGCCCGGATCTGTGTTGCCAGGAAGAC	1080
	Db		1021	GGCAAGTCTTGGGCGACGCTGTTTGGAGCCCGGATCTGTGTTGCCAGGAAGAC	1080
	QY		1081	AGGAAGCGGATGAAGATAGCATCAGAAGACGAAAGTTTCGGACAGTACAAAGAACGCT	1140
	Db		1081	AGGAAGCGGATGAAGATAGCATCAGAAGACGAAAGTTTCGGACAGTACAAAGAACGCT	1140
	QY		1141	GATGTTACGAAGCCCCGTTTCGTTCAGAACACATGTTATCCAGATGACATCCATCAAG	1200

D	b		1141	GATGTAGCAAGCGCCGGTTTCCTGCAGACACACATGATGCCAGATGACATCATCAAG	1260
Q	y		1201	AAACGAAGATCCCCAGATGATGAACCTGTTATACCTTACCAGTGAGGGCCGTGAGACTTAT	1260
D	b		1201	AAACGAAGATCCCCAGATGATGAACCTGTTATACCTTACCAGTGAGGGCCGTGAGACTTAT	1260
Q	y		1261	GAATGCTGTTGAGAGTCAAGAAGTCCTCGAAGTATGACAGTACCTTCTCAGCACACA	1320
D	b		1261	GAATGCTGTTGAGAGTCAAGAAGTCCTCGAAGTATGACAGTACCTTCTCAGCACACA	1320
Q	y		1321	ATTGAAACGTTACAGGCCAACAGCAACAGCAGCAGCACACGACTTACTTTCAGAAACA	1376
D	b		1321	ATTGAAACGTTACAGGCCAACAGCAACAGCAGCAGCACACGACTTACTTTCAGAAACA	1376
RESULT 9					
AAx58574					
ID	AAx58574 standard; cDNA; 1347 BP.				
XX					
AC	AAx58574;				
XX					
DT	16-AUG-1999 (first entry)				
XX					
DE	Human cell regulatory protein p63, isoform huTap63 gamma, CDNA.				
KW	Cell regulatory protein; p63; huTap63 gamma; Tap63 gamma; human;				
KW	cancer; tumour suppressor; cell cycle control; apoptosis;				
KW	cell proliferation; cell differentiation; therapy; ss.				
OS	Homo sapiens.				
XX					
FH	Key Location/Qualifiers				
FT	misc_difference 1254				
FT	/*tag= a				
FT	/note= "this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering given in the specification for this sequence"				
FT					
FN	WO9919357-A2.				
XX					
PD	22-APR-1999.				
XX					
PF	02-OCT-1998; 98WO-US21992.				
XX					
PR	29-MAY-1998; 98US-0087216.				
PR	15-OCT-1997; 97US-0062076.				
XX					
PA	(HARD) HARVARD COLLEGE.				
PI	McKeon F, Yang A;				
XX					
DR	WPI; 1999-277595/23.				
P-	PSDB; AAy05955.				
XX					
PT	New isolated p63 cell regulatory protein for, e.g. treatment of tumours				
XX					
PS	Claim 1; Fig 11; 161pp; English.				
XX					
CC	The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosome position 3q27-29. At least 6 different isotypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are				

Db	721	ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC	780
Qy	925	ACGACAGCTCTGTACAAATTTTCATGTGTAACAGCAGATTGCTGTGAGGAGATGAACCGCGCT	984
Db	781	ACGACAGCTCTGTACAAATTTTCATGTGTAACAGCAGATTGCTGTGAGGAGATGAACCGCGCT	840
Qy	985	CCAAATTTTAATCATTTGTTACTCTGGAAACACAGAGATGGCAAGTCCCTGGGCGCAGCGTCG	1044
Db	841	CCAAATTTTAATCATTTGTTACTCTGGAAACACAGAGATGGCAAGTCCCTGGGCGCAGCGTCG	900
Qy	1045	TTTGAGGCCCGGATCTGTGCTTGCCACAGGAAGACACAGGAGGCGGATGAAGATAGCATC	1104
Db	901	TTTGAGGCCCGGATCTGTGCTTGCCACAGGAAGACACAGGAGGCGGATGAAGATAGCATC	960
Qy	1105	AGAAAGCAGCAAGTTTCGGACAGCTACAAAGAACCGTGTATGGTACGAAGCGCCGCTTTCGT	1164

DB 561 AGAAAGCAGCAAGTATTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCGTTTCGT 1020

DB 1021 CAGAACACATGGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1080

QY	1225	CTGTTATACATTACCAGTGAGGGCCGGTGGAGACTTATGAAATGCTGTGGAAGATCAAAGAG	128
Db	1081	CTGTTATACATTACCAGTGAGGGCCGGTGGAGACTTATGAAATGCTGTGGAAGATCAAAGAG	1140
QY	1285	TCCTTGAACATCATGCAGTACCTTCCTCAGCACACAATTTGAAAGCTACAGGCAACAGCAA	1344
Db	1141	TCCTTGAACATCATGCAGTACCTTCCTCAGCACACAATTTGAAAGCTACAGGCAACAGCAA	1200
QY	1345	CAGCAGCAGCACACAGCACTTTACTTTCAGAAACATCTCCTTTTCAGGCTGCTTCAGGAATGAG	1404
Db	1201	CAGCAGCAGCACACAGCACTTTACTTTCAGAAACATCTCCTTTTCAGGCTGCTTCAGGAATGAG	1260
QY	1405	CTTGTGGAGCCCGGAGAGAAATCTCCAAAACAATCTGACGCTCTTTTTCAGACATTTCCAAG	1464
Db	1261	CTTGTGGAGCCCGGAGAGAAATCTCCAAAACAATCTGACGCTCTTTTTCAGACATTTCCAAG	1320
QY	1465	CCCCCAACCGATCAGTGATCCCATAG	1491
Db	1321	CCCCCAACCGATCAGTGATCCCATAG	1347
RESULT 10			
AAZ43913			
ID AAZ43913 standard; cDNA; 4846 BP.			
XX	AC	AAZ43913;	
XX	AC	AAZ43913;	
XX	14-MAR-2000	(first entry)	
DT	XX	Human KET cDNA.	
XX	DE		
XX	OS		
KW	XX	KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;	
KW	XX	p53 family; angiogenic; cytotoxic; cancer; human; ss.	
XX	OS		
XX	OS	Homo sapiens.	
PN	XX	W09961610-A2.	
XX	PN		
PD	XX	02-DEC-1999.	
XX	XX		
PF	XX	25-MAY-1999; 99WO-DE01557.	
XX	XX		
PR	XX	25-MAY-1998; 98DE-1022985.	
XX	XX		
PA	XX	(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.	
XX	XX		
PI	XX	Paul D, Augustin M, Schmale H, Bamberger C;	
XX	XX		
DR	XX	WPI; 2000-062710/05.	
DR	XX	P-PSDB; AAY50997.	
XX	XX		

RESULT 10
AAZ43913
ID AAZ43913 standard: CDNA: 4846 BP.

XX
AC
AAZ43913.

XX
DT 14-MAR-2000 (first entry)

XX DE Human KET cDNA.

XX KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;
KW p53 family; angiogenic; cytotoxic; cancer; human; ss.
KW p53 family; angiogenic; cytotoxic; cancer; human; ss.
XX KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

XX
XX
QS Homo sapiens.

XX
PN W09961610-22

XX
PD
02-DEC-1999

XX
DE 75-MAY-1980. 00W0-DE01557

XX
DD
75-MAY-1000
0000-103000

XX

[illegible][illegible]

DR P-PSDB; AAY50997.

PT New KET-encoding nucleic acid and related proteins, for diagnosis and
 treatment of tumors -
 XX
 PS Claim 3; Page 23-26; 28pp; German.
 XX
 CC This invention describes a novel KET-encoding nucleic acid (I) and its
 CC fragments, variants and mutants which has anticancer activity. (I)
 CC encodes a protein, (II), involved in control of the cell cycle and
 CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
 CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
 CC detect (I) in biological samples, specifically angiogenic tumor tissue,
 CC including (I) sequences that have a homozygotic deletion and (b) to
 CC detect presence or absence of human chromosome 3q27 or murine chromosome
 CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor
 CC suppressor, particularly in tumors where an alteration in the wild-type
 CC p53 allele has not been identified. (I) and (II) may also be used for
 CC development of specific cytotoxic agents and for predicting the risk of
 CC developing cancer. This sequence represents the human KET cDNA sequence
 CC described in the method of the invention.
 XX
 SQ Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;
 XX
 Query Match 45.3%; Score 1275; DB 21; Length 4846;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 102 CCCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACA 161
 Db 102 CCCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACA 161
 QY 162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC 221
 Db 162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC 221
 QY 222 TATATGTCAGTTCAGCCCATGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGC 281
 Db 222 TATATGTCAGTTCAGCCCATGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGC 281
 QY 282 GACAAACAGATTGAGATTAGCATGGAATCTATCCGATCCAGAGCTCGGACCTGAGTGA 341
 Db 282 GACAAACAGATTGAGATTAGCATGGAATCTATCCGATCCAGAGCTCGGACCTGAGTGA 341
 QY 342 CCCATGTGGCCAGTACAGAACCTGGGGCTCCTGAACAGCATGGACAGCAGATTCA 401
 Db 342 CCCATGTGGCCAGTACAGAACCTGGGGCTCCTGAACAGCATGGACAGCAGATTCA 401
 QY 402 GAACGGCTCCTCTCCACCATGCTTATACAGACAGACGCGCAGACAGCGTCAAGC 461
 Db 402 GAACGGCTCCTCTCCACCATGCTTATACAGACAGACGCGCAGACAGCGTCAAGC 461
 QY 462 GCCTCGCCCTACGACAGCCAGCTCCACCTCGATGCTCTCTCCATCACCCTGCAAT 521
 Db 462 GCCTCGCCCTACGACAGCCAGCTCCACCTCGATGCTCTCTCCATCACCCTGCAAT 521
 QY 522 CCCTCTCAACCGACTACCCAGCGCGGCGACAGTTTCGACGTGTCTTCCAGCAGTCGAG 581
 Db 522 CCCTCTCAACCGACTACCCAGCGCGGCGACAGTTTCGACGTGTCTTCCAGCAGTCGAG 581
 QY 582 CACCGCCAAAGTCGGCCACCTGGACGCTATTCACCTGAAGTGAAGAACTCTACTGCCAAT 641
 Db 582 CACCGCCAAAGTCGGCCACCTGGACGCTATTCACCTGAAGTGAAGAACTCTACTGCCAAT 641
 QY 642 TGCAGAGATGCCCATCCAGATCAAGTGTATGACCCACCTCCTCAGGGAGCTGTTAT 701
 Db 642 TGCAGAGATGCCCATCCAGATCAAGTGTATGACCCACCTCCTCAGGGAGCTGTTAT 701
 QY 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCC 761
 Db 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCC 761
 QY 762 CAACCATGAGTGCAGCCGTGAATTCACAGGAGGACAGATTGCCCTCCTAGTCAATTGAT 821
 Db 762 CAACCATGAGTGCAGCCGTGAATTCACAGGAGGACAGATTGCCCTCCTAGTCAATTGAT 821

QY 822 TCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCCATCAGCAAGACAGAG 881
 Db 822 TCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCCATCAGCAAGACAGAG 881
 QY 882 TGTGCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTCACGACAGCTTTGTACAA 941
 Db 882 TGTGCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTCACGACAGCTTTGTACAA 941
 QY 942 TTTTCATGCTGAACAGCAGTGTGTGGAGGGATGAACCCCGTCCCAATTTAATCATTTGT 1001
 Db 942 TTTTCATGCTGAACAGCAGTGTGTGGAGGGATGAACCCCGTCCCAATTTAATCATTTGT 1001
 QY 1002 TACTCTGGAACCCAGAGATGGGCAAGTCTCTGGCCGACGCTGTTTGAAGCCCGGATCTG 1061
 Db 1002 TACTCTGGAACCCAGAGATGGGCAAGTCTCTGGCCGACGCTGTTTGAAGCCCGGATCTG 1061
 QY 1062 TGTCTGCCAGGAGAGACAGAGGCGGATGAAGATAGCATCAGAAACAGCAAGTTTC 1121
 Db 1062 TGTCTGCCAGGAGAGACAGAGGCGGATGAAGATAGCATCAGAAACAGCAAGTTTC 1121
 QY 1122 GGACAGTCAAAAGAACGCTGATGGTACGAAGCCCGCTTTCGTCAGAACACACATGGTAT 1181
 Db 1122 GGACAGTCAAAAGAACGCTGATGGTACGAAGCCCGCTTTCGTCAGAACACACATGGTAT 1181
 QY 1182 CCAGATGACATCCATCAAGAACGAAGATCCCGAGATGAAGTGTATATCTTACCAGT 1241
 Db 1182 CCAGATGACATCCATCAAGAACGAAGATCCCGAGATGAAGTGTATATCTTACCAGT 1241
 QY 1242 GAGGGCCCTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301
 Db 1242 GAGGGCCCTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301
 QY 1302 GTACCTTCCTCAGCACACAATTTGAACGTACAGGCAACAGCAAGCAGCAGCAGCA 1361
 Db 1302 GTACCTTCCTCAGCACACAATTTGAACGTACAGGCAACAGCAAGCAGCAGCAGCA 1361
 QY 1362 CTTACTTCAGAAACA 1376
 Db 1362 CTTACTTCAGAAACA 1376
 RESULT 11
 AAC66031
 ID AAC66031 standard; cDNA; 4849 BP.
 XX
 AC AAC66031;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE Human lung cancer-associated cDNA p63 isoform 5.
 XX
 KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061612-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000WO-US08896.
 XX
 PR 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Fan L;
 XX

DR WPI; 2000-628399/60.
XX P-PSDB; AAB11361.
PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
in a patient -
PS Claim 25a; Page 240-242; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
XX Sequence 4849 BP; 1377 A; 1076 C; 988 G; 1407 T; 1 other;
SQ
Query Match 45.38; Score 1275; DB 21; Length 4849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
102 CCCAGCTCATTTCTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCACAGAGCACACA 161
102 CCCAGCTCATTTCTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCACAGAGCACACA 161
162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACGCC 221
162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACGCC 221
222 TATATGTCAGTTCAGCCCATTTGACTTGAATTTGTGGATGAACCATCAGAAAGATGTGC 281
222 TATATGTCAGTTCAGCCCATTTGACTTGAATTTGTGGATGAACCATCAGAAAGATGTGC 281
282 GACAAACAGATTGAGATTAGCATGGAGTGTATCCGATCGAGGACTCGGACCTGAGTGA 341
282 GACAAACAGATTGAGATTAGCATGGAGTGTATCCGATCGAGGACTCGGACCTGAGTGA 341
342 CCCCATGTGGCCACAGTACAGAACCTGGGGCTCCTGAACAGCATGGACAGCAGATTCA 401
342 CCCCATGTGGCCACAGTACAGAACCTGGGGCTCCTGAACAGCATGGACAGCAGATTCA 401
402 GAAGGGCTCTCTGTCACAGCTCCCTATACACAGACACCGCGAGACAGCGTCACGGC 461
402 GAAGGGCTCTCTGTCACAGCTCCCTATACACAGACACCGCGAGACAGCGTCACGGC 461
462 GCCCTGCCCTTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCGCAT 521
462 GCCCTGCCCTTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCGCAT 521
522 CCCCTCCACACAGCTACCCAGCCCGCAGTTTCGAGCTGTCCTTCCAGCAGTCGAG 581
522 CCCCTCCACACAGCTACCCAGCCCGCAGTTTCGAGCTGTCCTTCCAGCAGTCGAG 581
582 CACCGCCCAAGTCGCCACCTGGAGGTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641
582 CACCGCCCAAGTCGCCACCTGGAGGTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641
642 TGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTGTAT 701
642 TGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTGTAT 701
702 CCGCGCCATGCTGTCTACAAAAAGGTGACAGCTCACGGAGGTGTGTAAGCGGTGCC 761
702 CCGCGCCATGCTGTCTACAAAAAGGTGACAGCTCACGGAGGTGTGTAAGCGGTGCC 761
762 CAACCATGAGCTGAGCGGTGAATTCACAGGGGACAGATTGCCCTCTAGTCAATTTGAT 821
|||||

Db 762 CAACCATGAGCTGAGCGGTGAATTAACAGGGGACAGATTGCCCTCTAGTCAATTTGAT 821
Qy 822 TCGAGTAGAGGGGAACAGCCATGCCAGTAGTATGTAAGATCCCATCACAGGAACAGACAG 881
Db 822 TCGAGTAGAGGGGAACAGCCATGCCAGTAGTATGTAAGATCCCATCACAGGAACAGACAG 881
Qy 882 TGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTCACGACAGTCTTTGTACAA 941
Db 882 TGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTCACGACAGTCTTTGTACAA 941
Qy 942 TTTTCATGTATACAGCAGTGTGTGGAGGATGAACCGCGCTCCATTTTAATCATTTGT 1001
Db 942 TTTTCATGTATACAGCAGTGTGTGGAGGATGAACCGCGCTCCATTTTAATCATTTGT 1001
Qy 1002 TACTCTGGAACACAGAGATGGCAAGTCTCTGGCGGACGCTGCTTTGAGGCCCGGATCTG 1061
Db 1002 TACTCTGGAACACAGAGATGGCAAGTCTCTGGCGGACGCTGCTTTGAGGCCCGGATCTG 1061
Qy 1062 TGTCTGCCCCAGGAAGACAGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTC 1121
Db 1062 TGTCTGCCCCAGGAAGACAGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTC 1121
Qy 1122 GGACAGTACAAAGAACCGGTGATGTACGAACGCCCTTTCTCTCAGACACACATGGTAT 1181
Db 1122 GGACAGTACAAAGAACCGGTGATGTACGAACGCCCTTTCTCTCAGACACACATGGTAT 1181
Qy 1182 CCAGATGACATCCATCAAGAAACCAAGATCCCATGATGATGAATCTTTATCTTACCACT 1241
Db 1182 CCAGATGACATCCATCAAGAAACCAAGATCCCATGATGATGAATCTTTATCTTACCACT 1241
Qy 1242 GAGGGCGGTGAGACTTATGAATGCTGTGTAAGATCAAGAGTCCCTTGGAACTCATGCA 1301
Db 1242 GAGGGCGGTGAGACTTATGAATGCTGTGTAAGATCAAGAGTCCCTTGGAACTCATGCA 1301
Qy 1302 GTACCTTCCCTCAGCACACATTTGAAGCTGACAGCAACAGCAGCAGCAGCAGCAGCA 1361
Db 1302 GTACCTTCCCTCAGCACACATTTGAAGCTGACAGCAACAGCAGCAGCAGCAGCAGCA 1361
Qy 1362 CTTACTTCAGAAACA 1376
Db 1362 CTTACTTCAGAAACA 1376
RESULT 12
ABL49250
ID ABL49250 standard; cDNA; 4849 BP.
XX ABL49250;
AC ABL49250;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human p53 homologue isoform, p63 (L530S) cDNA sequence SEQ ID NO:335.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response; ss.
XX
OS Homo sapiens.
XX
EN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-US21065.
XX
PR 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
 XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 DR WPI: 2002-090513/12.
 DR P-PSDB; ABB74993.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2; Page 317-318; 374pp; English.
 XX
 CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 4849 BP; 1377 A; 1076 C; 988 G; 1407 T; 1 other;

Query Match 45.3%; Score 1275; DB 24; Length 4849;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CCCAGCTCATTTCTCTGGAAAGAAAGTTATTACCGATCCACCATGTCACAGACACACA 161
 DB 102 CCCAGCTCATTTCTCTGGAAAGAAAGTTATTACCGATCCACCATGTCACAGACACACA 161
 QY 162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACGCC 221
 DB 162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACGCC 221
 QY 222 TATATGTTAGTTCAGGCCCATTCAGTTGACCTTGTGGATGACCATCAGAAAGATGGTGC 281
 DB 222 TATATGTTAGTTCAGGCCCATTCAGTTGACCTTGTGGATGACCATCAGAAAGATGGTGC 281
 QY 282 GACAAACAGATTGAGATTAGCATGAGTCTATCCGATGCAGGACTCGGACCTGAGTGA 341
 DB 282 GACAAACAGATTGAGATTAGCATGAGTCTATCCGATGCAGGACTCGGACCTGAGTGA 341
 QY 342 CCCATGTGSCCAGCTACAGAACCTGGGGCTCTGTAACAGATGGACAGAGATCA 401
 DB 342 CCCATGTGSCCAGCTACAGAACCTGGGGCTCTGTAACAGATGGACAGAGATCA 401
 QY 402 GAACGGCTCCTCGTCCACCATGTCCTTATACACAGACACGCGCAGAACAGGTCACGGC 461
 DB 402 GAACGGCTCCTCGTCCACCATGTCCTTATACACAGACACGCGCAGAACAGGTCACGGC 461
 QY 462 GCCCTCGCCCTAGCCAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGGCCAT 521
 DB 462 GCCCTCGCCCTAGCCAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGGCCAT 521
 QY 522 CCCTCCCAACACCGACTACCCAGGCCGCGACAGTTTCGACGTCCTTCCACAGTCGAG 581
 DB 522 CCCTCCCAACACCGACTACCCAGGCCGCGACAGTTTCGACGTCCTTCCACAGTCGAG 581
 QY 582 CACCGCCAGTCGGCCACCTGGACGCTATTCCACTGAAGTGAAGAACTCTACTGCCAAAT 641
 DB 582 CACCGCCAGTCGGCCACCTGGACGCTATTCCACTGAAGTGAAGAACTCTACTGCCAAAT 641
 QY 642 TCAAGAGATGCCCATTCAGATCAAGTGTATGACCCACCTCTCTCAGGGAGCTGTAT 701
 DB 642 TCAAGAGATGCCCATTCAGATCAAGTGTATGACCCACCTCTCTCAGGGAGCTGTAT 701
 QY 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCACCTCAGGAGGTGGTGAACCGGTGCC 761
 DB 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCACCTCAGGAGGTGGTGAACCGGTGCC 761

QY 762 CAACCATGAGCTGAGCCGTGAATTCACAGAGGAGACAGATTGCCCTCCTAGTCATTGTAT 821
 DB 762 CAACCATGAGCTGAGCCGTGAATTCACAGAGGAGACAGATTGCCCTCCTAGTCATTGTAT 821
 QY 822 TCAGTAGAGGGGAACAGCCATGCCAGATATGTAGAGATGCCATCACAGGAACAGAG 881
 DB 822 TCAGTAGAGGGGAACAGCCATGCCAGATATGTAGAGATGCCATCACAGGAACAGAG 881
 QY 882 TGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTCACACAGCTCTTGTACAA 941
 DB 882 TGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTCACACAGCTCTTGTACAA 941
 QY 942 TTTTCATGCTTAACAGCAGTTGTTGGAGGGATGAACCCGCTGCCAATTTAATCATTTGT 1001
 DB 942 TTTTCATGCTTAACAGCAGTTGTTGGAGGGATGAACCCGCTGCCAATTTAATCATTTGT 1001
 QY 1002 TACTCTGGAAACCCAGAGATGGGCAAGTCTCTGGCCGACGCTGTTTGGGCCCGGATCTG 1061
 DB 1002 TACTCTGGAAACCCAGAGATGGGCAAGTCTCTGGCCGACGCTGTTTGGGCCCGGATCTG 1061
 QY 1062 TGTCTGCCAGGAGACAGAGGAGGCGGATGAAGATAGCATCAGAAAGCAAGTTTC 1121
 DB 1062 TGTCTGCCAGGAGACAGAGGAGGCGGATGAAGATAGCATCAGAAAGCAAGTTTC 1121
 QY 1122 GGACAGTACAAAGAACGGTGTGATGACGAAGCGCGGTTTCGTCAGAACACACATGGTAT 1181
 DB 1122 GGACAGTACAAAGAACGGTGTGATGACGAAGCGCGGTTTCGTCAGAACACACATGGTAT 1181
 QY 1182 CCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAACCTTATCTTACCAGT 1241
 DB 1182 CCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAACCTTATCTTACCAGT 1241
 QY 1242 GAGGGCCGCTGAGACTTATGAATGCTTGTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301
 DB 1242 GAGGGCCGCTGAGACTTATGAATGCTTGTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301
 QY 1302 GTACCTTCCTCAGCACACAAATTTGAAACGCTACAGGCAACAGCAACAGCAGCACCAGCA 1361
 DB 1302 GTACCTTCCTCAGCACACAAATTTGAAACGCTACAGGCAACAGCAACAGCAGCACCAGCA 1361
 QY 1362 CTTACTTCAGAAACA 1376
 DB 1362 CTTACTTCAGAAACA 1376

RESULT 13
 AAX58573

ID AAX58573 standard; cDNA; 1551 BP.

XX AAX58573;

AC AAX58573;

DT 16-AUG-1999 (first entry)

XX Human cell regulatory protein p63, isoform huTap63 beta, cDNA.

DE Cell regulatory protein; p63; huTap63 beta; Tap63 beta; human;

XX cancer; tumour suppressor; cell cycle control; apoptosis;

XX cell proliferation; cell differentiation; therapy; ss.

OS Homo sapiens.

XX WO9919357-A2.

XX 22-APR-1999.

XX 02-OCT-1998; 98WO-US21992.

XX 29-MAY-1998; 98US-0087216.

XX 15-OCT-1997; 97US-0062076.

XX (HARD) HARVARD COLLEGE.

XX McKeon F, Yang A;

PI

XX WPI; 1999-277595/23.
DR P-PSDB; AAY05954.
XX
PT New isolated p63 cell regulatory protein for, e.g. treatment of
tumours
PS
PS Claim 1; Fig 10; 161pp; English.
XX
CC The present invention concerns the discovery of a new family of
cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as deltaN and TA forms, where the deltaN form lacks the
CC transactivation domain. The present sequence represents a cDNA
CC clone encoding human TAp63 beta. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAY58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;
Query Match 43.8%; Score 1232; DB 20; Length 1551;
Best Local Similarity 100.08; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ATGTCACAGAGCAGACACAGCAAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
DB 1 ATGTCACAGAGCAGACACAGCAAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
QY 205 GATTTCTGGAAACAGCCTATATGTTTCAGTCCAGCCCATGACTTGAACCTTTGGATGAA 264
DB 61 GATTTCTGGAAACAGCCTATATGTTTCAGTCCAGCCCATGACTTGAACCTTTGGATGAA 120
QY 265 CCATCAGAGAGATGGCGACAAACAGATTAGATTAGCATGGAGTGTATCCGATGAG 324
DB 121 CCATCAGAGAGATGGCGACAAACAGATTAGATTAGCATGGAGTGTATCCGATGAG 180
QY 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACTCGGGGCTCTCTGAACAGC 384
DB 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACTCGGGGCTCTCTGAACAGC 240
QY 385 ATGGACACAGCAGATTCAGAACGGCTCTCTGCTCCACAGTCCCTATAACACAGACACGCG 444
DB 241 ATGGACACAGCAGATTCAGAACGGCTCTCTGCTCCACAGTCCCTATAACACAGACACGCG 300
QY 445 CAGAACAGCTCAGCGGCGCTCGCCCTACGCACAGCCACGCTCAGCTTCGATGCTCTC 504
DB 301 CAGAACAGCTCAGCGGCGCTCGCCCTACGCACAGCCACGCTCAGCTTCGATGCTCTC 360
QY 505 TCTCCATCAGCCGCTCTCCCTCCAAACAGCAGTACCCAGCCGCGCAGTTTCGAGGTG 564
DB 361 TCTCCATCAGCCGCTCTCCCTCCAAACAGCAGTACCCAGCCGCGCAGTTTCGAGGTG 420
QY 565 TCCTTCCAGCAGTCGAGCAGCCGCAAGTCGCGCCACCTGGAGCTATTCACCTGAAGTGAAG 624

DB 421 TCCTTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACCTGGACGATATTCACCTGAAGTGAAG 480
QY 625 AAACCTACTGCTCCAAATTCGAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 584
DB 481 AAACCTACTGCTCCAAATTCGAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 540
QY 685 CCTCAGGAGCTGTTATCCGGCCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGCGAG 744
DB 541 CCTCAGGAGCTGTTATCCGGCCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGCGAG 600
QY 745 GTGGTGAAGCGGTGCCCCAACCATCAGCTGAGCCCTGTAATTCACAGAGGACAGATGCC 804
DB 601 GTGGTGAAGCGGTGCCCCAACCATCAGCTGAGCCCTGTAATTCACAGAGGACAGATGCC 660
QY 805 CCTCCTACTGCTATTCGATTCGAGTACAGGGGACACCCATGCCACCTATGTAGAAATGCC 864
DB 661 CCTCCTACTGCTATTCGATTCGAGTACAGGGGACACCCATGCCACCTATGTAGAAATGCC 720
QY 865 ATCAGAGGACAGAGTGTGCTGTACTCTTATGAGCCACCCAGGTTGGCAGTGAATTC 924
DB 721 ATCAGAGGACAGAGTGTGCTGTACTCTTATGAGCCACCCAGGTTGGCAGTGAATTC 780
QY 925 AGCAGAGTCTGTACAAATTTATGTTACAGCAGTGTGTTGGAGGATGAACCGCGCT 984
DB 781 AGCAGAGTCTGTGTACAAATTTATGTTACAGCAGTGTGTTGGAGGATGAACCGCGCT 840
QY 985 CCAATTTTAATCATTTTACTCTGGAACACACAGAGATGGCAAGTCTCTGGCCGACGCTGC 1044
DB 841 CCAATTTTAATCATTTTACTCTGGAACACACAGAGATGGCAAGTCTCTGGCCGACGCTGC 900
QY 1045 TTTGAGGCGCGATCTGTCTTGGCCAGGACAGAGAGAGGCGGATGAAGATAGCATC 1104
DB 901 TTTGAGGCGCGATCTGTCTTGGCCAGGACAGAGAGAGGCGGATGAAGATAGCATC 960
QY 1105 AGAAGACAGCAAGTTTTCGACAGTACAAAGAACGGTGTGTGACGAGGCGGCTTTCGT 1164
DB 961 AGAAGACAGCAAGTTTTCGACAGTACAAAGAACGGTGTGTGACGAGGCGGCTTTCGT 1020
QY 1165 CAGAACACACATGTTATCCAGATGACATCCATCAAGAACAGAGATCCCCAGATGATGA 1224
DB 1021 CAGAACACACATGTTATCCAGATGACATCCATCAAGAACAGAGATCCCCAGATGATGA 1080
QY 1225 CTGTTATCTACTTACCAGTGGGCGCTGAGACTTATGAAATGCTTGAAGATCAAGAG 1284
DB 1081 CTGTTATCTACTTACCAGTGGGCGCTGAGACTTATGAAATGCTTGAAGATCAAGAG 1140
QY 1285 TCCCTGGAACTCATGCTGCTTCCCTCAGCACACAATTTGAACGCTAGAGGCAACAGCA 1344
DB 1141 TCCCTGGAACTCATGCTGCTTCCCTCAGCACACAATTTGAACGCTAGAGGCAACAGCA 1200
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTTCAGAAACA 1376
DB 1201 CAGCAGCAGCAGCAGCAGCTTACTTTCAGAAACA 1232
RESULT 14
AAC66033
ID AAC66033 standard; cDNA; 1551 BP.
XX
AC AAC66033;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human lung cancer-associated cDNA p63 isoform 7.
XX
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX vaccine; detection; ss.
XX
OS Homo sapiens.
XX
PN WO200061612-A2.
XX

PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000WO-US08896.
 XX
 PR 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Wang T, Fan L;
 PI WPI; 2000-628399/60.
 XX P-PSDB; AAB11363.
 DR
 DR Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 XX
 PS Claim 25a; Page 242-243; 261pp; English.
 XX
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2, and then administered to the patient to inhibit
 CC development of cancer.
 XX
 XX Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;
 SQ
 - Query Match 43.8%; Score 1232; DB 21; Length 1551;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 145 ATGTCCAGAGCAGACAGACAATGATTCCTCAGTCCAGAGTTTCCAGCATATCTGG 204
 Db 1 ATGTCCAGAGCAGACAGACAATGATTCCTCAGTCCAGAGTTTCCAGCATATCTGG 204
 QY 205 GATTTCTCGGACAGCCTATATGTTTCAGTTCAGCCCATGACTTGAACCTTTGGATGAA 264
 Db 61 GATTTCTCGGACAGCCTATATGTTTCAGTTCAGCCCATGACTTGAACCTTTGGATGAA 264
 QY 265 CCATCAGAAGATGTGGCAAAACAGATTGAGATTAGCATGACATGATCCGCATGCAG 324
 Db 121 CCATCAGAAGATGTGGCAAAACAGATTGAGATTAGCATGACATGATCCGCATGCAG 324
 QY 325 GACTCGGACCTGAGTGACCCATGTGGCCACAGATACAGAACCTGGGGCTCTCGAACAGC 384
 Db 181 GACTCGGACCTGAGTGACCCATGTGGCCACAGATACAGAACCTGGGGCTCTCGAACAGC 384
 QY 385 ATGACACAGCAGATTGAGAACGGCTCTCTGTCACACAGTCCCTATTAACACAGACACCGC 444
 Db 241 ATGACACAGCAGATTGAGAACGGCTCTCTGTCACACAGTCCCTATTAACACAGACACCGC 444
 QY 445 CAGAACAGCTGACGGCCCTCGCTAGCCACAGCCAGCTCCACCTTCGATGCTCTC 504
 Db 301 CAGAACAGCTGACGGCCCTCGCTAGCCACAGCCAGCTCCACCTTCGATGCTCTC 504
 QY 505 TCTCCATACCGCCCATCCCTCCCAACACCGACTACCCAGCCCGCAGAGTTTCGAGGTG 564
 Db 361 TCTCCATACCGCCCATCCCTCCCAACACCGACTACCCAGCCCGCAGAGTTTCGAGGTG 564
 QY 565 TCTTCCAGCTGACGACCGCCCAAGTGGCCACCTGGAGTATTCAGTGAAGTGAAG 624
 Db 421 TCTTCCAGCTGACGACCGCCCAAGTGGCCACCTGGAGTATTCAGTGAAGTGAAG 624

QY 625 AAATCTACTGCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
 Db 481 AAATCTACTGCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540
 QY 685 CCTCAGGAGCTGTTATTCGCGCCATGCTGTCTACAAAAGCTGAGCACGTGACGGAG 744
 Db 541 CCTCAGGAGCTGTTATTCGCGCCATGCTGTCTACAAAAGCTGAGCACGTGACGGAG 600
 QY 745 GTGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGACAGATTGCC 804
 Db 601 GTGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGACAGATTGCC 660
 QY 805 CCTCTAGTCTATTGATTGAGTAGAGGGAACAGCCATGCCAGTATGAGAAGATGCC 864
 Db 661 CCTCTAGTCTATTGATTGAGTAGAGGGAACAGCCATGCCAGTATGAGAAGATGCC 720
 QY 865 ATCAGAGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924
 Db 721 ATCAGAGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 780
 QY 925 ACGACAGTCTTGTACAAATTCATGCTGTACACAGCTGTGTGGAGGGATGAACCGCGT 984
 Db 781 ACGACAGTCTTGTACAAATTCATGCTGTACACAGCTGTGTGGAGGGATGAACCGCGT 840
 QY 985 CCAATTTTAACTGTTTACTCTGGAACCAAGAGATGGCAAGTCTTGGCGCGAGCTGC 1044
 Db 841 CCAATTTTAACTGTTTACTCTGGAACCAAGAGATGGCAAGTCTTGGCGCGAGCTGC 900
 QY 1045 TTTGAGGCCCGGATCTGCTGTGCGCCAGAGACAGAGATGGCGGCGAGTATGAGTATC 1104
 Db 901 TTTGAGGCCCGGATCTGCTGTGCGCCAGAGACAGAGATGGCGGCGAGTATGAGTATC 960
 QY 1105 AGAAGACAGCAAGTTTCGGAGCAGTACAAAGAACCGTGTGATGAGAACCGCCGTTTCGT 1164
 Db 961 AGAAGACAGCAAGTTTCGGAGCAGTACAAAGAACCGTGTGATGAGAACCGCCGTTTCGT 1020
 QY 1165 CAGAACACACATGGTATCCAGATCAGATCCATCAAGAAACAGATGATGATGATGAA 1224
 Db 1021 CAGAACACACATGGTATCCAGATCAGATCCATCAAGAAACAGATGATGATGATGAA 1080
 QY 1225 CTGTTATCTTACCAGTGAAGGGCGGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG 1284
 Db 1081 CTGTTATCTTACCAGTGAAGGGCGGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG 1140
 QY 1285 TCCCTGGAACCTGATGAGTACCTTCTCAGCAGACAAATTCAGAGTACAGGCAACAGCAA 1344
 Db 1141 TCCCTGGAACCTGATGAGTACCTTCTCAGCAGACAAATTCAGAGTACAGGCAACAGCAA 1200
 QY 1345 CAGCAGCAGCAGCAGCAGTACTTTCAGAAACA 1376
 Db 1201 CAGCAGCAGCAGCAGCAGTACTTTCAGAAACA 1232

RESULT 15
 ABL49252
 ID ABL49252 standard; cDNA; 1551 BP.
 XX
 AC ABL49252;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human p53 homologue isoform, p63 (L530S) cDNA sequence SEQ ID NO:337.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW Immune response; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX WPI: 2002-090513/12.
DR P-PSDB; ABB74995.
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX Example 2; Page 319; 374pp; English.
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
XX invention.
XX Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;
SQ

Query Match 43.8%; Score 1232; DB 24; Length 1551;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ATGTCAGAGCAGACAGACAAATGCTCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
DB 1 ATGTCAGAGCAGACAGACAAATGCTCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
QY 205 GATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACATTTGTGGATGAA 264
DB 61 GATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACATTTGTGGATGAA 120
QY 265 CCATCAGAAGATGTTGGACAAACAAAGATTGAGATTAGCATGGAGTGTATCCGCATGCGAG 324
DB 121 CCATCAGAAGATGTTGGACAAACAAAGATTGAGATTAGCATGGAGTGTATCCGCATGCGAG 180
QY 325 GACTCGGACCTGAGTGACCCCATGTCGCCAGTACAGAACCTGGGGCTCCTCAACAGC 384
DB 181 GACTCGGACCTGAGTGACCCCATGTCGCCAGTACAGAACCTGGGGCTCCTCAACAGC 240
QY 385 ATGGACAGCAGATTACAGAGCGGCTCTCGTCCACAGTCCCTATACACAGACACGCG 444
DB 241 ATGGACAGCAGATTACAGAGCGGCTCTCGTCCACAGTCCCTATACACAGACACGCG 300
QY 445 CAGAACAGGTCAGGCGCGCTCGCCCTACGCACAGCCAGTCCACCTTCGATGCTCTC 504
DB 301 CAGAACAGGTCAGGCGCGCTCGCCCTACGCACAGCCAGTCCACCTTCGATGCTCTC 360
QY 505 TCTCCATCAGCGCATCCCTCCACACAGCAGTACCCAGCGCCGCGACGTTTCGAGGTG 564
DB 361 TCTCCATCAGCGCATCCCTCCACACAGCAGTACCCAGCGCCGCGACGTTTCGAGGTG 420
QY 565 TCCTTCCAGCAGTCGAGCAGCGCCCAAGTCGCCACCTGGAGTATTCACCTGAAGTGAAG 624
DB 421 TCCTTCCAGCAGTCGAGCAGCGCCCAAGTCGCCACCTGGAGTATTCACCTGAAGTGAAG 480
QY 625 AACTCTACTGCCAAATTTGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
|||||

Db 481 AACTCTACTGCCAAATTTGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540
QY 685 CCTCAGGAGAGCTGTTATCCGCGCATGCTCTACAAAAAGCTGAGCAGCTCAGCGAG 744
DB 541 CCTCAGGAGAGCTGTTATCCGCGCATGCTCTACAAAAAGCTGAGCAGCTCAGCGAG 600
QY 745 GTGGTGAAGCGGTCGCCCAACCATGAGCTGAGCCGTGAATTCACAGGAGGACAGATTGCC 804
DB 601 GTGGTGAAGCGGTCGCCCAACCATGAGCTGAGCCGTGAATTCACAGGAGGACAGATTGCC 660
QY 805 CCTCCTAGTCAATTTGATTCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCC 864
DB 661 CCTCCTAGTCAATTTGATTCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCC 720
QY 865 ATCAGAGGAACAGAGAGTGTCTGTACCTTATGAGCCACCCAGGTTGGCAGCTGAATTC 924
DB 721 ATCAGAGGAACAGAGAGTGTCTGTACCTTATGAGCCACCCAGGTTGGCAGCTGAATTC 780
QY 925 ACAGAGTCTTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGGAGGATGAACCGCGT 984
DB 781 ACAGAGTCTTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGGAGGATGAACCGCGT 840
QY 985 CCAATTTTAAATCATGTTACTCTCGAAACACAGAGATGGGCAAGTCTCTGGGCGGAGCTGCG 1044
DB 841 CCAATTTTAAATCATGTTACTCTCGAAACACAGAGATGGGCAAGTCTCTGGGCGGAGCTGCG 900
QY 1045 TTTGAGGCGCGGATCTGTGCTTGGCCAGGAAGACAGAGAGGCGGATGAAGATAGCATC 1104
DB 901 TTTGAGGCGCGGATCTGTGCTTGGCCAGGAAGACAGAGAGGCGGATGAAGATAGCATC 960
QY 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGGTGATGTGTAAGACGCGCCGTTTCGT 1164
DB 961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGGTGATGTGTAAGACGCGCCGTTTCGT 1020
QY 1165 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCGAGATGATGAA 1224
DB 1021 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCGAGATGATGAA 1080
QY 1225 CTGTTATACTTACCAGTGAGGGCGGTGAGACTTATGAAATGCTCTTGAAGATCAAGAG 1284
DB 1081 CTGTTATACTTACCAGTGAGGGCGGTGAGACTTATGAAATGCTCTTGAAGATCAAGAG 1140
QY 1285 TCCCTGGAACATCATGCACTACCTTCTCCTCAGCACACAATTTGAACGTACAGCAACAGCAA 1344
DB 1141 TCCCTGGAACATCATGCACTACCTTCTCCTCAGCACACAATTTGAACGTACAGCAACAGCAA 1200
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376
DB 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232

Search completed: June 28, 2003, 08:12:09
Job time : 605 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 08:01:58 ; Search time 399 Seconds
(without alignments)
10476.708 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1055720 seqs, 742224136 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2111440

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

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- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2816	100.0	2816	10	US-09-850-716A-333
3	2816	100.0	2816	10	US-09-897-778-333
4	1376	48.9	2270	10	US-09-735-705-333
5	1376	48.9	2270	10	US-09-850-716A-332
6	1376	48.9	2270	10	US-09-897-778-332
7	1275	45.3	4849	10	US-09-735-705-335
8	1275	45.3	4849	10	US-09-850-716A-335
9	1275	45.3	4849	10	US-09-897-778-335
10	1232	43.8	1551	10	US-09-735-705-337
11	1232	43.8	1551	10	US-09-850-716A-337
12	1232	43.8	1551	10	US-09-897-778-337
13	1026	36.4	1386	10	US-09-735-705-336
14	1026	36.4	1386	10	US-09-850-716A-336
15	1026	36.4	1386	10	US-09-897-778-336
16	975	34.6	2082	9	US-10-274-874-1
17	975	34.6	2082	10	US-09-735-705-334
18	975	34.6	2082	10	US-09-850-716A-334
19	975	34.6	2082	10	US-09-897-778-334

20	826	29.3	4655	10	US-09-735-705-151	Sequence 151, App
21	826	29.3	4655	10	US-09-850-716A-151	Sequence 151, App
22	826	29.3	4655	10	US-09-897-778-151	Sequence 151, App
23	822	29.2	2820	10	US-09-735-705-331	Sequence 331, App
24	822	29.2	2820	10	US-09-850-716A-331	Sequence 331, App
25	822	29.2	2820	10	US-09-897-778-331	Sequence 331, App
26	25	0.9	491	9	US-09-918-995-7344	Sequence 7344, App
27	25	0.9	491	10	US-09-783-590-494	Sequence 494, App
28	25	0.9	646	9	US-10-106-698-517	Sequence 517, App
29	25	0.9	90442	9	US-10-105-637-1	Sequence 1, Appli
30	24	0.9	329	9	US-09-803-719-555	Sequence 555, App
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32	24	0.9	439	9	US-09-918-995-13871	Sequence 13871, A
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ALIGNMENTS

RESULT 1

US-09-735-705-333
Sequence 333, Application US/09735705
Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455G14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 333
LENGTH: 2816
TYPE: DNA
ORGANISM: Homo sapiens
US-09-735-705-333

Query Match 100.0%; Score 2816; DB 10; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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; Sequence 333, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-333
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Query Match 100.0%; Score 2816; DB 10; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1141 GATGTAAGGCGCGCTTTGCTGACAGACACATGTTATCCAGATGACATCATCAAG 1200
1141 GATGTAAGGCGCGCTTTGCTGACAGACACATGTTATCCAGATGACATCATCAAG 1200
1201 AAACGAAGATCCCGAGATGATGAATTTATCTTACCAGTGAGGGCGCTGAGACTTAT 1260
1201 AAACGAAGATCCCGAGATGATGAATTTATCTTACCAGTGAGGGCGCTGAGACTTAT 1260
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCACTACCTTCTCAGCACACA 1320

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1741 GAACCACTGT 1800
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1801 GAAAGGGCACTTAAGATGTTTATGGAACCCCTTTCTGTCTCTCTCTCTCTCTCTCTCT 1860
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1981 CCCTTTTAAATGCTGCTGATTAATTAATTTGCAAGTAGTAAGAAACGAGGTTGCAAGTG 2040
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2221 CATGAACCCCTGGAGAGCTACTACAAAGAACTGTTGTTGGCCCCCATAGCAGGTGA 2280
2281 CTCATTTTGTGCTTTTAAATAGAAAGCAAAATCCACCCAGTAATATTGCCCTTAGCTAGT 2340
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2341 TGTTTACCATTTTCAAAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAATAATCTGTGAT 2400

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2701 CACAGCACTGTTTCTGTCACCAAGACAATGATTTCTGTTTATGAGGCTGTTGCTT 2760
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2761 TTTGCGATGTTGATTTTAAATTTCAATAAATCTTTGCAATCTTGGTTTAAAGAAA 2816
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RESULT 4

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US-09-735-705-332
; Sequence 332, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Fongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-332
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Query Match 48.9%; Score 1376; DB 10; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTCAAACTTCACGGTGTGCCACCT 60
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Db
61 ACAGTACTCCCTGACCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
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Db
181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240
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1081 AGAAGCGGATGAAGATAGCATCAGAAAGACAGAGTTTCGACAGTACAAAGACGGT 1140
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1141 GATGGTACCAAGCGCCGTTTCGTGAGAACACATGTTATCCAGATGACATCCATCAAG 1200
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1141 GATGGTACCAAGCGCCGTTTCGTGAGAACACATGTTATCCAGATGACATCCATCAAG 1200
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1201 AAACGAAGATCCCCAGATGATGAATGTTTATATTACCAGTGGGGCGGTGAGACTTAT 1260
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; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-332

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Query Match	48.9%	Score 1376;	DB 10;	Length 2270;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1376;	Conservative 0;			
QY 1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTGAAACTTCACGSGTGGCCACCT	60		
DB				
QY 1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTGAAACTTCACGSGTGGCCACCT	60		
DB				
QY 61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120		
DB				
QY 61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120		
DB				
QY 121	AAAGAAAGTTATTACGATCCACCATTCCAGACACACAGACAAATGAATTCCTCAGT	180		
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QY 121	AAAGAAAGTTATTACGATCCACCATTCCAGACACACAGACAAATGAATTCCTCAGT	180		
DB				
QY 181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGACAGCCCTATATGTTTCAGTTCAGCCC	240		
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QY 181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGACAGCCCTATATGTTTCAGTTCAGCCC	240		
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QY 241	ATTGACTTGAATTTGTGGATGAACCATCAGAAGATGTCGCAACACAGATGAGATT	300		
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DB				
QY 421	AGTCCTATAACACAGACACCGGCACAGCGTACGCGCCCTCGCCCTACGCACAG	480		
DB				
QY 421	AGTCCTATAACACAGACACCGGCACAGCGTACGCGCCCTCGCCCTACGCACAG	480		
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QY 481	CCAGCTCCACCTTCGATGCTCTCTCTCCATCACCGGCATCCCTCCACACCGACTAC	540		
DB				
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DB				
QY 601	TGGACGPTATCCACTGAACTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCCATC	660		
DB				
QY 601	TGGACGPTATCCACTGAACTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCCATC	660		
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QY 661	CAGATCAAGGTGATGACCCCACTCCTCAGGAGCTGTTATCCCGGCATTCGCTGCTAC	720		
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DB				
QY 721	AAAAAGCTGAGCAGTTCAGGAGTGTGAAGCGTGTCCCAACATGAGCTGAGCCGT	780		
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QY 721	AAAAAGCTGAGCAGTTCAGGAGTGTGAAGCGTGTCCCAACATGAGCTGAGCCGT	780		
DB				
QY 781	GAAATTCACGAGGACAGATTGCCCTCTCTAGTTCATTTGATTCGAGTAGAGGGGAACAG	840		
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QY 781	GAAATTCACGAGGACAGATTGCCCTCTCTAGTTCATTTGATTCGAGTAGAGGGGAACAG	840		
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QY 841	CATGCCCAAGTATGTAGAAGATCCCATCACAGGACAGAGTGTGCTGATCTATGAG	900		
DB				

Db	841	CATGCCACGATATGAGAAGATCCATCAGGAAGACAGAGTGTGCTGGTACTCTTATGAG	900
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Db	901	CCACCCACGTTGGCACTCAATTCACGACAGTCCTGTGACATTTTCATGTGTAACACGAGT	960
Qy	961	TGTTGTTGGAGGATGAACCGCGCTCCAAATTTTAATCATTTTACTCTGGAACACAGAGAT	1020
Db	961	TGTTGTTGGAGGATGAACCGCGCTCCAAATTTTAATCATTTTACTCTGGAACACAGAGAT	1020
Qy	1021	GGCAAGTCTCTGGGCGGACGCTGCTTTGAGGCCGCGATCTGTGCTTGCCTCCAGGAAGAC	1080
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Qy	1081	AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTCAACAAGAAGCGT	1140
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Qy	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCAGTACCTTCTCCAGCACACA	1320
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Qy	1321	ATTGAAACGTTACAGGCAACAGCAACAGCAGCAGCACCAGCACTTACTTCAGAAACA	1376
Db	1321	ATTGAAACGTTACAGGCAACAGCAACAGCAGCAGCACCAGCACTTACTTCAGAAACA	1376

RESULT 7

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US-09-735-705-335
; Sequence 335, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-335

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	Query Match	45.3%	Score 1275;	DB 10;	Length 4849;
	Best Local Similarity	100.0%;	Prod. No. 0;		
	Matches 1275;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTCGAACAGCC 221
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282 GACAAACAAAGATTGAGATTAGCATGGAGTGTATCCGATGAGGACTCGGACCTGAGTGA 341
342 CCCCATGTGGCCACAGTACAGAACCTGGGCTCCTGAACAGCATGGACACAGATTCATCA 401
342 CCCCATGTGGCCACAGTACAGAACCTGGGCTCCTGAACAGCATGGACACAGATTCATCA 401
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762 CAACCATGAGTGAAGCGTGAATTCACGAGGGACAGATTGCCCTCCTAGTCAATTTGAT 821
762 CAACCATGAGTGAAGCGTGAATTCACGAGGGACAGATTGCCCTCCTAGTCAATTTGAT 821
822 TCAGTAGAGGGGAACAGCCATGCCAGTATGTAGAAGATCCCATCAGGAAGACACAGAG 881
822 TCAGTAGAGGGGAACAGCCATGCCAGTATGTAGAAGATCCCATCAGGAAGACACAGAG 881
882 TGTGCTGTTACCTTTATGAGCCACCCAGTTGGCACTGAATTCAGCAGTCTTTGTACAA 941
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942 TTTTCATGTTAAGACAGTGTGTGGAGGATGAACCGCGCTCCAATTTTAATCATTTGT 1001
942 TTTTCATGTTAAGACAGTGTGTGGAGGATGAACCGCGCTCCAATTTTAATCATTTGT 1001
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1062 TGTCTGGAACACAGAGATGGCAAGTCTTGGCGGAGCGTCTTGGAGCCCGGATCTG 1121
1062 TGTCTGGAACACAGAGATGGCAAGTCTTGGCGGAGCGTCTTGGAGCCCGGATCTG 1121
1122 GGACAGTACAAGAACGGTGTATGATGAGAGCCCGCTTTCGTGAGACACACATGGTAT 1181
1122 GGACAGTACAAGAACGGTGTATGATGAGAGCCCGCTTTCGTGAGACACACATGGTAT 1181
1182 CCAGATGACATCCATCAAGAAACGAGATCCCGAGATGATGAATGTTTATCTACTACCAAGT 1241
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1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301

1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCA 1301
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1362 CTTACTTCCAGAAACA 1376
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RESULT 8
US-09-850-716A-335
; Sequence 335, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-335

Query Match 45.3%; Score 1275; DB 10; Length 4849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CCCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGCAGCACA 161
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DB 462 GCCCTGCGCTTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCGGCAT 521
QY 522 CCCCTCCAACACCGACTACCCAGCCCGCACAGTTTCCAGCTGCTCTTCCAGCAGTCGAG 581
DB 522 CCCCTCCAACACCGACTACCCAGCCCGCACAGTTTCCAGCTGCTCTTCCAGCAGTCGAG 581
QY 582 CACCGCCCAAGTCGGCCACCTGGAGCTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641
DB 582 CACCGCCCAAGTCGGCCACCTGGAGCTATTCACCTGAAGAACTCTACTGCCAAAT 641


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QY 642 TCGAAGACATGCCCATCCAGATCAAGGTGATGACCCACCTCTCCAGGAGCTGTAT 701
Db 642 TCGAAGACATGCCCATCCAGATCAAGGTGATGACCCACCTCTCCAGGAGCTGTAT 701
QY 702 CCGGCCATGCTGCTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGTGGCC 761
Db 702 CCGGCCATGCTGCTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGTGGCC 761
QY 762 CAACCATGAGTGAAGCGTGAATTCACGAGGAGACAGATTGCCCTCTCCAGTGTAT 821
Db 762 CAACCATGAGTGAAGCGTGAATTCACGAGGAGACAGATTGCCCTCTCCAGTGTAT 821
QY 822 TCGAGTAGAGGGAACAGCATGCCCATGATGAGAGATCCATCAGAGGAAGACAG 881
Db 822 TCGAGTAGAGGGAACAGCATGCCCATGATGAGAGATCCATCAGAGGAAGACAG 881
QY 882 TGTGCTGTACCTTATGAGCCACCCAGGTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
Db 882 TGTGCTGTACCTTATGAGCCACCCAGGTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
QY 942 TTTTCATGTGTACAGCAGTGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
Db 942 TTTTCATGTGTACAGCAGTGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
QY 1002 TACTCTGGAACACAGATGGCAAGTCTTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
Db 1002 TACTCTGGAACACAGATGGCAAGTCTTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
QY 1062 TGTCTGCCAGGACAGACAGAGGCGGATGAGATAGCATCAGAAAGCAGCAAGTTTC 1121
Db 1062 TGTCTGCCAGGACAGACAGAGGCGGATGAGATAGCATCAGAAAGCAGCAAGTTTC 1121
QY 1122 GACAGTACAAGACCGTGTGTAGGAGCGCGCTTTCGTCAGACACACATGGTAT 1181
Db 1122 GACAGTACAAGACCGTGTGTAGGAGCGCGCTTTCGTCAGACACACATGGTAT 1181
QY 1182 CCAGATGACATCCATCAGAACAGATCCAGATGATGAATCTTATCTTACCTAG 1241
Db 1182 CCAGATGACATCCATCAGAACAGATCCAGATGATGAATCTTATCTTACCTAG 1241
QY 1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAATCA 1301
Db 1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAATCA 1301
QY 1302 GTACCTTCTCAGCACACATTCAGACGTACAGGCAACAGCAGCAGCAGCAGCA 1361
Db 1302 GTACCTTCTCAGCACACATTCAGACGTACAGGCAACAGCAGCAGCAGCAGCA 1361
QY 1362 CTACTCTCAGAAACA 1376
Db 1362 CTACTCTCAGAAACA 1376
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RESULT 9

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US-09-897-778-335
; Sequence 335, Application US/0989778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-335
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Query Match

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Best Local Similarity 45.3%; Score 1275; DB 10; Length 4849;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 CCAGCTCAATTCCTCTTGGAAAGAAAGTTATTACGATCCACCATGTCCAGAGACACA 161
Db 102 CCAGCTCAATTCCTCTTGGAAAGAAAGTTATTACGATCCACCATGTCCAGAGACACA 161
QY 162 GACAAATGAATTCCTCAGTCCAGAGGTTTTCAGCATATCTGGGATTTTCTGGAACGCC 221
Db 162 GACAAATGAATTCCTCAGTCCAGAGGTTTTCAGCATATCTGGGATTTTCTGGAACGCC 221
QY 222 TATATGTTCAAGTTCAGCCCATTTGACTTGAACCTTTGTGATGACCATCAGAGATGTTGC 281
Db 222 TATATGTTCAAGTTCAGCCCATTTGACTTGAACCTTTGTGATGACCATCAGAGATGTTGC 281
QY 282 GACAAACAGATGAGATTAGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTGA 341
Db 282 GACAAACAGATGAGATTAGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTGA 341
QY 342 CCCCATGTGGCCACAGTACAGCAACCTGGGGCTCTGAAACAGCATGACGAGATTCAC 401
Db 342 CCCCATGTGGCCACAGTACAGCAACCTGGGGCTCTGAAACAGCATGACGAGATTCAC 401
QY 402 GAAGGCTCTCTGTCACAGGATCCCTATACACAGACACGCGCAGAACAGCGTCACGGC 461
Db 402 GAAGGCTCTCTGTCACAGGATCCCTATACACAGACACGCGCAGAACAGCGTCACGGC 461
QY 462 GCCCTGCGCTTACACAGAGCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCTAT 521
Db 462 GCCCTGCGCTTACACAGAGCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCTAT 521
QY 522 CCCCCTCAACACAGGACTACCCAGGCGCGACAGTTTCGACGTTCTCCAGCAGTCGAG 581
Db 522 CCCCCTCAACACAGGACTACCCAGGCGCGACAGTTTCGACGTTCTCCAGCAGTCGAG 581
QY 582 CACGCGCAAGTGGCCACCTGGAGCTATTCCACTGAACCTGAAGAACTCTACTGCCAAT 641
Db 582 CACGCGCAAGTGGCCACCTGGAGCTATTCCACTGAACCTGAAGAACTCTACTGCCAAT 641
QY 642 TCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTTAT 701
Db 642 TCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTTAT 701
QY 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGTGGCC 761
Db 702 CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGTGGCC 761
QY 762 CAACCATGAGCTGAGCGGTGAATTCACAGAGGACAGATTGCCCTCTCTAGTCAATTGAT 821
Db 762 CAACCATGAGCTGAGCGGTGAATTCACAGAGGACAGATTGCCCTCTCTAGTCAATTGAT 821
QY 822 TCGAGTAGAGGGAACAGCATGCCCATGATGAGAGATCCATCAGAGGAAGACAGAG 881
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QY 882 TGTGCTGTACCTTATGAGCCACCCAGGTGGGAGGATGAACCGCGTCCAAATTTAATCA 941
Db 882 TGTGCTGTACCTTATGAGCCACCCAGGTGGGAGGATGAACCGCGTCCAAATTTAATCA 941
QY 942 TTTTCATGTGTACAGCAGTGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
Db 942 TTTTCATGTGTACAGCAGTGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATGT 1001
QY 1002 TACTCTGGAACACAGATGGCAAGTCTTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1061
Db 1002 TACTCTGGAACACAGATGGCAAGTCTTGGGAGGATGAACCGCGTCCAAATTTAATCATGT 1061
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RESULT 11

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US-09-850-716A-337
: Sequence 337, Application US/09850716A
: Patent No. US20020115139A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
:
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
:
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 337
:
: LENGTH: 1551.
:
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: US-09-850-716A-337

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Query Match	43.8%;	Score 1232;	DB 10;	Length 1551;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	145	ATGTC	CCAGCAGACACAGACAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG	204
Db	1	ATGTC	CCAGCAGACACAGACAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG	60
QY	205	GATTTTCTGGAACGCTTATGTTCAGTTCAGCCCATTTGACTTGAACTTTGGGATGAA	264	
Db	61	GATTTTCTGGAACGCTTATGTTCAGTTCAGCCCATTTGACTTGAACTTTGGGATGAA	120	
QY	265	CCATCAGAAGATGGTGACAAAACAAGATTGAGATTAGCATGACGCTATCCCGCATGCGAG	324	
Db	121	CCATCAGAAGATGGTGACAAAACAAGATTGAGATTAGCATGACGCTATCCCGCATGCGAG	180	
QY	325	GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGTCTCTGAAACAGC	384	
Db	181	GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGTCTCTGAAACAGC	240	
QY	385	ATGACCACGAGATTTCAGAAGCGGCTCCTGTCACACAGTCCCTATTAACACAGACACGCGG	444	
Db	241	ATGACCACGAGATTTCAGAAGCGGCTCCTGTCACACAGTCCCTATTAACACAGACACGCGG	300	
QY	445	CAGAACAGCGTCAAGGCGGCTCGCCCTAGCCACAGCCAGCTCCACCTTCGATGCTCTC	504	
Db	301	CAGAACAGCGTCAAGGCGGCTCGCCCTAGCCACAGCCAGCTCCACCTTCGATGCTCTC	360	
QY	505	TCTCCATCACC	CGCCATCCCTCCAAACACCGACTACCCAGGCCCCCAGTTTCGACGTG	564
Db	361	TCTCCATCACC	CGCCATCCCTCCAAACACCGACTACCCAGGCCCCCAGTTTCGACGTG	420
QY	565	TCCTTCCAGCGT	CGAGCACCGCCCAAGTGGGCCACTGGAGCTATTCACACGAACTGAG	624
Db	421	TCCTTCCAGCGT	CGAGCACCGCCCAAGTGGGCCACTGGAGCTATTCACACGAACTGAG	480
QY	625	AAACTCTACTG	CCAAATTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT	684
Db	481	AAACTCTACTG	CCAAATTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT	540
QY	685	CCTCAGGAGCTG	TTATCCGCGCCATGCGTCTCATAAAAAGCTGAGCAGCTCAGCGAG	744
Db	541	CCTCAGGAGCTG	TTATCCGCGCCATGCGTCTCATAAAAAGCTGAGCAGCTCAGCGAG	600
QY	745	GTGGTGAAGCGG	TGCCCAACCATGAGCTGAGCGGTGAATTCAACGAGGGACAGATTGCG	804
Db	601	GTGGTGAAGCGG	TGCCCAACCATGAGCTGAGCGGTGAATTCAACGAGGGACAGATTGCG	860
QY	805	CCTCCTAGTCA	TTTGTTCAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCC	864
Db	661	CCTCCTAGTCA	TTTGTTCAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCC	720

RESULT 12

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US-09-897-778-337
; Sequence 337, Application US/09897778
; Patent No..US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R. R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-337

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	Query Match	43.8%	Score 1232	DB 10	Length 1551
	Best Local Similarity	100.0%	Pred. No. 0		
	Matches 1232	Conservative	Mismatches 0	Indels 0	Gaps 0
QY	145	ATGTCCTCCAGAGCACACAGACAAATGAATTCCTCAGTCACAGAGTTTCCACGCATATCTGG	204		
Db	1	ATGTCCTCCAGAGCACACAGACAAATGAATTCCTCAGTCACAGAGTTTCCACGCATATCTGG	60		
QY	205	GATTTCCTGGAAACAGCCCTATATCTTCAGTTCAGCCCCATTGACTTGAACCTTTGTGGATGAA	264		

Db 61 GATTTCGTGAACAGCCTATATGTTCAAGTTCAGCCCATTTGACTTGAACCTTTGTGGATGAA 120
QY 265 CCATCAGAGATGTCGGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCGATCGAG 324
Db 121 CCATCAGAAGATGTCGGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCGATCGAG 180
QY 325 GACTCGGACCTGAGTCAGCCCATGTCGCCACAGTACAGAACCTGGGGCTCCTGAACAGC 384
Db 181 GACTCGGACCTGAGTCAGCCCATGTCGCCACAGTACAGAACCTGGGGCTCCTGAACAGC 240
QY 385 ATGACACGACAGATTGAGAACGGCTCTCTGTCACACAGTCCCTATAACACAGACACGCG 444
Db 241 ATGACACGACAGATTGAGAACGGCTCTCTGTCACACAGTCCCTATAACACAGACACGCG 300
QY 445 CAGAACAGCTGACAGCGGCTGCGCTTACACAGCCAGCTCCACCTTCGATGCTCTC 504
Db 301 CAGAACAGCTGACAGCGGCTGCGCTTACACAGCCAGCTCCACCTTCGATGCTCTC 360
QY 505 TCTCCATCACCGCCATCCCTCCAAACACCTACCCAGCGCCGACAGTTTCGACGTG 564
Db 361 TCTCCATCACCGCCATCCCTCCAAACACCTACCCAGCGCCGACAGTTTCGACGTG 420
QY 565 TCTTCCAGCAGTCGAGACCGCAAGTCGGCCACCTGGAGCTATTCCACTGAACTGAAG 624
Db 421 TCTTCCAGCAGTCGAGACCGCAAGTCGGCCACCTGGAGCTATTCCACTGAACTGAAG 480
QY 625 AAATCTACTGCCAAATTCGAAACATGCCCCATCAGATCAAGATGATGACCCACCT 684
Db 481 AAATCTACTGCCAAATTCGAAACATGCCCCATCAGATCAAGATGATGACCCACCT 540
QY 685 CCTCAGGAGCTGTTATCCGGCCCATGCTGTCTACAAAAGCTGACAGCTCACGGAG 744
Db 541 CCTCAGGAGCTGTTATCCGGCCCATGCTGTCTACAAAAGCTGACAGCTCACGGAG 600
QY 745 GTGTGAAGCGGTGCCCAACCATGAGTCGAGCGCTGAATTCACAGGGGACAGATTGCC 804
Db 601 GTGTGAAGCGGTGCCCAACCATGAGTCGAGCGCTGAATTCACAGGGGACAGATTGCC 660
QY 805 CCTCCTAGCTATTGATTCGAGTAGAGGGACAGCCATGCCAGATGTAGAGATGCC 864
Db 661 CCTCCTAGCTATTGATTCGAGTAGAGGGAAACAGCCATGCCAGTATGTAGAGATGCC 720
QY 865 ATCAGAGAACACAGAGTGTCTGTATGAGCCACCCAGGTGGCACTGAATTC 924
Db 721 ATCAGAGAACACAGAGTGTCTGTATGAGCCACCCAGGTGGCACTGAATTC 780
QY 925 ACGACGTCTGTACAAATTCATGTGAACAGCAGTGTGTGGAGGATGAACCGCGT 984
Db 781 ACGACGTCTGTACAAATTCATGTGAACAGCAGTGTGTGGAGGATGAACCGCGT 840
QY 985 CCAATTTTAATCATTTGTTACTCTGSAACACAGAGATGGCAAGTCTTGGCCGCGCTGC 1044
Db 841 CCAATTTTAATCATTTGTTACTCTGSAACACAGAGATGGCAAGTCTTGGCCGCGCTGC 900
QY 1045 TTTGAGGCCCGGATCTGTCTGTCAGGAAGACAGAGAGGGCGGATGAAGATAGCATC 1104
Db 901 TTTGAGGCCCGGATCTGTCTGTCAGGAAGACAGAGAGGGCGGATGAAGATAGCATC 960
QY 1105 AGAAGCAGCAAGTTTCGGACAGTACAAAGACCGGTGATGTAGACGCGCCCTTTCGT 1164
Db 961 AGAAGCAGCAAGTTTCGGACAGTACAAAGACCGGTGATGTAGACGCGCCCTTTCGT 1020
QY 1165 CAGAACACATGATTCAGATGACATCCATCAAGAACAGATCCCAAGATGATGAA 1224
Db 1021 CAGAACACATGATTCAGATGACATCCATCAAGAACAGATCCCAAGATGATGAA 1080
QY 1225 CTGTTATACTTACCAAGTAGAGGGCGGTGAGACTTATGAAATGCTGTTGAAGTCAAGAG 1284
Db 1081 CTGTTATACTTACCAAGTAGAGGGCGGTGAGACTTATGAAATGCTGTTGAAGTCAAGAG 1140
QY 1285 TCCCTGGAACATCATGTCAGTACCTTCTCAGCACACAATTTGAACAGTACAGCAACAGCA 1344

Db 1141 TCCCTGGAACTCATGTCAGTACTTCTCAGCACACAATTTGAACGTACAGCAACAGCAA 1200
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232
RESULT 13
US-09-735-705-336
; Sequence 336, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 336
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-336

Query Match 36.4%; Score 1026; DB 10; Length 1386;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 GCCACAGTACACGAACTTGGGGCTCCTGAACAGATGACGACGAGATTCAGAACGGCTC 410
Db 42 GCCACAGTACACGAACTTGGGGCTCCTGAACAGATGACGACGAGATTCAGAACGGCTC 101
QY 411 CTCTGTCCACAGTCCCTATACACAGACCCGCGCAGAACGCTCAGCGGCGCTCGCC 470
Db 102 CTCTGTCCACAGTCCCTATACACAGACCCGCGCAGAACGCTCAGCGGCGCTCGCC 161
QY 471 CTAGCGACAGCCCGACGCTCCACCTTCGATGCTCTCTCCATCACCGCGCATCCCTCCAA 530
Db 162 CTAGCGACAGCCCGACGCTCCACCTTCGATGCTCTCTCCATCACCGCGCATCCCTCCAA 221
QY 531 CACGACGTACCCAGCGCGCACAGTTTCGAGCTGTCTTCCAGCAGTTCGAGCAGCGCAA 590
Db 222 CACGACGTACCCAGCGCGCACAGTTTCGAGCTGTCTTCCAGCAGTTCGAGCAGCGCAA 281
QY 591 GTCGGCCACCTGGAGCTATTCACCTGAACTGAAGAACTCTACTGCCAAATTCGAAAGAC 650
Db 282 GTCGGCCACCTGGAGCTATTCACCTGAACTGAAGAACTCTACTGCCAAATTCGAAAGAC 341
QY 651 ATGCCCATCCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATTCGGCGCAT 710
Db 342 ATGCCCATCCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATTCGGCGCAT 401
QY 711 GCCTGTCTACAAAAAGCTGACGCTCAGCGAGTGTGTGAAGCGGTGCCCAACCATGA 770
Db 402 GCCTGTCTACAAAAAGCTGACGCTCAGCGAGTGTGTGAAGCGGTGCCCAACCATGA 461
QY 771 GCTGAGCGGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCTATTGATTTCGAGTGA 830
Db 462 GCTGAGCGGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCTATTGATTTCGAGTGA 521

; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897, 778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-897-778-336

Query Match 36.4%; Score 1026; DB 10; Length 1386;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	351	GCCACAGTACACGAACCTGGGGCTCTCTGAACAGCATGGACCAGCAGATTGACAGCGCTC	410
Db	42	GCCACAGTACACGAACCTGGGGCTCTCTGAACAGCATGGACCAGCAGATTGACAGCGCTC	101
Qy	411	CTGCTCCACCAAGTCCCTATACACAGACGACGCGGCGAGACAGCGTACGGCGCCCTCGCC	470
Db	102	CTGCTCCACCAAGTCCCTATACACAGACGACGCGGCGAGACAGCGTACGGCGCCCTCGCC	161
Qy	471	CTAGGCACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA	530
Db	162	CTAGGCACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA	221
Qy	531	CACCGACTACCCAGGCGCGCACAGTTTCGAGTGTCTCTCCAGCAGTCGAGCAGCGCCAA	590
Db	222	CACCGACTACCCAGGCGCGCACAGTTTCGAGTGTCTCTCCAGCAGTCGAGCAGCGCCAA	281
Qy	591	GTGGGCACTGACGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	650
Db	282	GTGGGCACTGACGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	341
Qy	651	ATGCCCATCCAGTCAAGGTGATGACCCACCTCTCTCAGGAGCTGTTATCCGCGCAT	710
Db	342	ATGCCCATCCAGTCAAGGTGATGACCCACCTCTCTCAGGAGCTGTTATCCGCGCAT	401
Qy	711	GCCTGTCTACAAAAAGCTGAGCAGCTCACGGAGTGGTGAAGCGTGCCTCCCAACCATGA	770
Db	402	GCCTGTCTACAAAAAGCTGAGCAGCTCACGGAGTGGTGAAGCGTGCCTCCCAACCATGA	461
Qy	771	GCTGAGCCGTGAATTCACAGGAGCAGATTGCCCTCTCTAGTCATTTGATTCGAGTAGA	830
Db	462	GCTGAGCCGTGAATTCACAGGAGCAGATTGCCCTCTCTAGTCATTTGATTCGAGTAGA	521
Qy	831	GGGGAACAGCAGTCCCGAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGT	890
Db	522	GGGGAACAGCAGTCCCGAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGT	581
Qy	891	ACCTTATGAGCCACCCAGGTTGGCACTGTAATTCACGACAGTCTTGTACAAATTTCAATGTG	950
Db	582	ACCTTATGAGCCACCCAGGTTGGCACTGTAATTCACGACAGTCTTGTACAAATTTCAATGTG	641
Qy	951	TAACAGCAGTGTGTGGAGGGATGAACCCCGTCCAAATTTAATCAATTTACTCTGGA	1010
Db	642	TAACAGCAGTGTGTGGAGGGATGAACCCCGTCCAAATTTAATCAATTTACTCTGGA	701
Qy	1011	AACCCAGAGTGGCAAGTCTCTGGCGCAGCTGCTTGTAGGCGCGGATCTGTGCTTGCCTC	1070
Db	702	AACCCAGAGTGGCAAGTCTCTGGCGCAGCTGCTTGTAGGCGCGGATCTGTGCTTGCCTC	761
Qy	1071	AGGAAGAGACAGGAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTAC	1130

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Db	822	AAAGAACGGTGAATGGTAGAAGCCCGTTTCGTGCAAGACACACATGGTATCCAGATGAC	881
Qy	1191	ATCCATCAAGAAAGCAAGATCCCCAGATGATGAAGTGTATATCTTACCAGTGAGGGCGG	1250
Db	882	ATCCATCAAGAAAGCAAGATCCCCAGATGATGAAGTGTATATCTTACCAGTGAGGGCGG	941
Qy	1251	TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTCGAAGTCTATGCAAGTACCTTCC	1310
Db	942	TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTCGAAGTCTATGCAAGTACCTTCC	1001
Qy	1311	TCAGCACACAATTGAACAGTACAGGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGC	1370
Db	1002	TCAGCACACAATTGAACAGTACAGGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGC	1061
Qy	1371	GAACA 1376	
Db	1062	GAACA 1067	

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OM protein - protein search, using sw model

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(without alignments)
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Searched: 671580 seqs, 206047115 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	487	4 Q9H3D2	Q9h3d2 homo sapien
2	410	91.5	471	4 Q9NPH7	Q9nph7 homo sapien
3	410	91.5	516	4 Q9P1B7	Q9p1b7 homo sapien
4	410	91.5	555	4 Q9H3D3	Q9h3d3 homo sapien
5	410	91.5	641	4 Q75195	Q75195 homo sapien
6	410	91.5	680	4 Q9UE10	Q9ue10 homo sapien
7	410	91.5	680	4 Q9H3B4	Q9h3b4 homo sapien
8	379	84.6	393	4 Q75922	Q75922 homo sapien
9	341	76.1	416	4 Q9P1B6	Q9p1b6 homo sapien
10	341	76.1	461	4 Q9P1B5	Q9p1b5 homo sapien
11	341	76.1	461	4 Q9UP26	Q9up26 homo sapien
12	341	76.1	586	4 Q9P1B4	Q9p1b4 homo sapien
13	341	76.1	586	4 Q9UBV9	Q9ubv9 homo sapien
14	284	63.4	483	11 O88897	O88897 mus musculus
15	284	63.4	555	11 Q9QWZ0	Q9qwz0 mus musculus
16	284	63.4	680	11 O88898	O88898 mus musculus

17	272	60.7	586	4	O75080	O75080 homo sapien
18	269	60.0	356	4	O9UP74	O9up74 homo sapien
19	259	57.8	389	11	O88899	O88899 mus musculus
20	259	57.8	461	11	O9QWY9	O9qw9 mus musculus
21	259	57.8	586	11	O89097	O89097 mus musculus
22	256	57.1	501	4	O9H3P8	O9h3p8 homo sapien
23	248	55.4	393	11	O99JD9	O99jd9 rattus norv
24	248	55.4	461	11	O99JD6	O99jd6 rattus norv
25	248	55.4	470	11	O99JE1	O99je1 rattus norv
26	248	55.4	487	11	O99JE0	O99je0 rattus norv
27	248	55.4	538	11	O99JD7	O99jd7 rattus norv
28	248	55.4	555	11	O99JD8	O99jd8 rattus norv
29	248	55.4	586	11	O99JE2	O99je2 rattus norv
30	248	55.4	663	11	O99JE3	O99je3 rattus norv
31	248	55.4	680	11	O9JJP6	O9jjp6 rattus norv
32	220	49.1	232	4	O96KR0	O96kr0 homo sapien
33	137	30.6	582	13	O9DEC7	O9dec7 gallus gall
34	95	21.2	365	13	O98SW0	O98sw0 xenopus lae
35	22	4.9	450	4	O8TDY5	O8tdy5 homo sapien
36	22	4.9	587	4	O8TDY6	O8tdy6 homo sapien
37	22	4.9	641	13	O9W664	O9w664 barbus barb
38	20	4.5	514	11	O9CU77	O9cu77 mus musculus
39	20	4.5	590	11	O9JJF1	O9jjf1 mus musculus
40	20	4.5	631	11	O9JJF2	O9jjf2 mus musculus
41	18	4.0	497	11	O9WUJ0	O9wu0 mus musculus
42	15	3.3	44	6	O8WM08	O8wmq8 canis famil
43	14	3.1	228	5	O27918	O27918 mya arenari
44	14	3.1	265	13	O9W681	O9w681 oncorhynch
45	14	3.1	265	13	O9W682	O9w682 oncorhynch

ALIGNMENTS

RESULT 1

Q9H3D2 ID Q9H3D2 PRELIMINARY: PRT: 487 AA.
AC Q9H3D2; O76078;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE TA p63 gamma (P51 isoform TAP63GAMMA).
GN p63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 40-487 FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishloka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M., Ikawa S.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53.";
RL Nat. Med. 4:839-843(1998).
RN [4]
RP SEQUENCE OF 40-487 FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;

"Mutation and expression of the p51 gene in human lung cancer.";

RT Neoplasia 1:71-79(1999).

RL EMBL; AF124540; AAG45609.1; -

DR EMBL; AF124528; AAG45609.1; JOINED.

DR EMBL; AF124529; AAG45609.1; JOINED.

DR EMBL; AF124531; AAG45609.1; JOINED.

DR EMBL; AF124532; AAG45609.1; JOINED.

DR EMBL; AF124533; AAG45609.1; JOINED.

DR EMBL; AF124534; AAG45609.1; JOINED.

DR EMBL; AF124535; AAG45609.1; JOINED.

DR EMBL; AF075428; AAG62633.1; -

DR EMBL; AB016072; BAA32592.1; -

DR EMBL; AF116770; AAF43486.1; -

DR EMBL; AF116756; AAF43486.1; JOINED.

DR EMBL; AF116759; AAF43486.1; JOINED.

DR EMBL; AF116760; AAF43486.1; JOINED.

DR EMBL; AF116761; AAF43486.1; JOINED.

DR EMBL; AF116762; AAF43486.1; JOINED.

DR EMBL; AF116763; AAF43486.1; JOINED.

DR EMBL; AF116764; AAF43486.1; JOINED.

DR EMBL; AF116765; AAF43486.1; JOINED.

DR HSP; P04637; LYCS.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR PRODOM; PD002681; P53; 1.

DR PROSITE; PS00348; P53; UNKNOWN_1.

SQ SEQUENCE 487 AA; 55687 MW; 86CC865BDF2643DD CRC64;

Query Match 100.0%; Score 448; DB 4; Length 487;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60

DB 40 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99

QY 61 DSDLSPPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

DB 100 DSDLSPPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180

DB 160 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 219

QY 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240

DB 220 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 279

QY 241 ITGROSLVYPPEPPQVGTFTTVLNFMCNSCVGGMNRRPILIIIVTLETRDQVIGRRC 300

DB 280 ITGROSLVYPPEPPQVGTFTTVLNFMCNSCVGGMNRRPILIIIVTLETRDQVIGRRC 339

QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360

DB 340 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 399

QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKLLSACFRNE 420

DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKLLSACFRNE 459

QY 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448

DB 460 LVEPRRETQKQSDVFFRHSKPPNRSVYP 487

RESULT 2

Q9NPH7
ID Q9NPH7 PRELIMINARY; PRT; 471 AA.
AC Q9NPH7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

01-DEC-2001 (Tremblrel. 19, Last annotation update)

P51 isoform Tap63delta (P51 delta protein).

DE Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20388515; PubMed=10935472;

RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;

RA "Mutation and expression of the p51 gene in human lung cancer.";

RL Neoplasia 1:71-79(1999).

DR EMBL; AF116771; AAF61624.1; -

DR EMBL; AF116769; AAF43489.1; -

DR EMBL; AF116756; AAF43489.1; JOINED.

DR EMBL; AF116757; AAF43489.1; JOINED.

DR EMBL; AF116759; AAF43489.1; JOINED.

DR EMBL; AF116760; AAF43489.1; JOINED.

DR EMBL; AF116761; AAF43489.1; JOINED.

DR EMBL; AF116762; AAF43489.1; JOINED.

DR EMBL; AF116763; AAF43489.1; JOINED.

DR EMBL; AF116764; AAF43489.1; JOINED.

DR EMBL; AF116765; AAF43489.1; JOINED.

DR HSP; P04637; LYCS.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR PRODOM; PD002681; P53; 1.

DR PROSITE; PS00348; P53; UNKNOWN_1.

SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CB69 CRC64;

Query Match 91.5%; Score 410; DB 4; Length 471;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60

DB 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60

QY 61 DSDLSPPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

DB 61 DSDLSPPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180

DB 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180

QY 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240

DB 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240

QY 241 ITGROSLVYPPEPPQVGTFTTVLNFMCNSCVGGMNRRPILIIIVTLETRDQVIGRRC 300

DB 241 ITGROSLVYPPEPPQVGTFTTVLNFMCNSCVGGMNRRPILIIIVTLETRDQVIGRRC 300

QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360

DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360

QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410

DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410

RESULT 3

Q9P1B7
ID Q9P1B7 PRELIMINARY; PRT; 516 AA.
AC Q9P1B7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE P51 isoform Tap63beta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.
 RT "Mutation and expression of the p51 gene in human lung cancer."
 RL Neoplasia 1:71-79(1999).
 DR EMBL; AF116769; AAF43488.1; JOINED.
 DR EMBL; AF116756; AAF43488.1; JOINED.
 DR EMBL; AF116757; AAF43488.1; JOINED.
 DR EMBL; AF116759; AAF43488.1; JOINED.
 DR EMBL; AF116760; AAF43488.1; JOINED.
 DR EMBL; AF116761; AAF43488.1; JOINED.
 DR EMBL; AF116762; AAF43488.1; JOINED.
 DR EMBL; AF116763; AAF43488.1; JOINED.
 DR EMBL; AF116764; AAF43488.1; JOINED.
 DR EMBL; AF116765; AAF43488.1; JOINED.
 DR EMBL; AF116766; AAF43488.1; JOINED.
 DR EMBL; AF116767; AAF43488.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; UNKNOWN_1.
 DR PROSITE; PS00348; P53; UNKNOWN_1.
 SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 91.5%; Score 410; DB 4; Length 516;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 DB 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLVPEPQVGTEFTVLYNFCNCSVCGMNRRLIIVTLTETRDGQVLRRC 300
 DB 241 ITGROSVLVPEPQVGTEFTVLYNFCNCSVCGMNRRLIIVTLTETRDGQVLRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKKRSPDDE 360
 DB 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKKRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQHLLQK 410
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQHLLQK 410

RESULT 4
 Q9H3D3 ID Q9H3D3 PRELIMINARY; PRT; 555 AA.
 AC Q9H3D3; Q9UP27;
 DT 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE TA p63 beta.

GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities."
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hagihara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124539; AAG45608.1; JOINED.
 DR EMBL; AF124528; AAG45608.1; JOINED.
 DR EMBL; AF124529; AAG45608.1; JOINED.
 DR EMBL; AF124531; AAG45608.1; JOINED.
 DR EMBL; AF124532; AAG45608.1; JOINED.
 DR EMBL; AF124533; AAG45608.1; JOINED.
 DR EMBL; AF124534; AAG45608.1; JOINED.
 DR EMBL; AF124535; AAG45608.1; JOINED.
 DR EMBL; AF124536; AAG45608.1; JOINED.
 DR EMBL; AF124537; AAG45608.1; JOINED.
 DR EMBL; AF075432; AAC62637.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; UNKNOWN_1.
 DR PROSITE; PS00348; P53; UNKNOWN_1.
 SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBACBE CRC64;

Query Match 91.5%; Score 410; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 DB 40 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
 QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
 QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 DB 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
 QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 220 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 279
 QY 241 ITGROSVLVPEPQVGTEFTVLYNFCNCSVCGMNRRLIIVTLTETRDGQVLRRC 300
 DB 280 ITGROSVLVPEPQVGTEFTVLYNFCNCSVCGMNRRLIIVTLTETRDGQVLRRC 339
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKKRSPDDE 360
 DB 340 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKKRSPDDE 399
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQHLLQK 410
 DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQHLLQK 449

RESULT 5
 O75195 ID O75195 PRELIMINARY; PRT; 641 AA.
 AC O75195;

```
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE P51 isoform TAP63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawa A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53.";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AB016073; BAA32593.1; -
DR EMBL; AF116769; AAF43487.1; -
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 91.5%; Score 410; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIEMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIEMDCIRMQ 60
QY 61 DSDLSPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120
DB 61 DSDLSPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSLVLPYPPQVQGTFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300
DB 241 ITGROSLVLPYPPQVQGTFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300
QY 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRRSPDDE 360
DB 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRRSPDDE 360
```

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DB 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410

RESULT 6
Q9UE10 PRELIMINARY; PRT; 680 AA.
AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE KET protein.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE AND KERATINOCYTE CULTURE;
RX MEDLINE=99018225; PubMed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";
RL Mamm. Genome 9:899-902(1998).
DR EMBL; Y16961; CAA76562.1; -
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 91.5%; Score 410; DB 4; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIEMDCIRMQ 60
DB 40 MSQSTQTNFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIEMDCIRMQ 99
QY 61 DSDLSPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120
DB 100 DSDLSPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 159
QY 121 SPSPALPSNTDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPALPSNTDYPGPHSFQVDFVQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSLVLPYPPQVQGTFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300
DB 280 ITGROSLVLPYPPQVQGTFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 339
QY 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRRSPDDE 360
DB 340 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 449
```

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RESULT 7
Q9H3D4
ID Q9H3D4 PRELIMINARY; PRT: 680 AA.
AC Q9H3D4: Q9UP28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TA p63 alpha.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Raghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Raghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075429; AAC62634.1; -
DR EMBL; AF116770; AAF43490.1; -
DR EMBL; AF116758; AAF43490.1; JOINED.
DR EMBL; AF116759; AAF43490.1; JOINED.
DR EMBL; AF116760; AAF43490.1; JOINED.
DR EMBL; AF116761; AAF43490.1; JOINED.
DR EMBL; AF116762; AAF43490.1; JOINED.
DR EMBL; AF116763; AAF43490.1; JOINED.
DR EMBL; AF116764; AAF43490.1; JOINED.
DR EMBL; AF116765; AAF43490.1; JOINED.
DR EMBL; AF124540; AAG45612.1; -
DR EMBL; AF124530; AAG45612.1; JOINED.
DR EMBL; AF124531; AAG45612.1; JOINED.
DR EMBL; AF124532; AAG45612.1; JOINED.
DR EMBL; AF124533; AAG45612.1; JOINED.
DR EMBL; AF124534; AAG45612.1; JOINED.
DR EMBL; AF124535; AAG45612.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 91.5%; Score 410; DB 4; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFEFLSPVEFHWDPLEOPICSVOPIDLNFDVDEPSEDGATNKIELSMDCIRMQ 60
DB 40 MSQSTQTNFEFLSPVEFHWDPLEOPICSVOPIDLNFDVDEPSEDGATNKIELSMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSDVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTPP 180
DB 160 SPSPAIPNTDYPGPHSDVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTPP 219
QY 181 POGAVIRAMPYVYKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVEGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVYKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPQVGVTEFTVLYNFMNCSSCGVMNRRLIIVTLTETRDGQVLGRRC 300
DB 280 ITGRQSVLPYEPQVGVTEFTVLYNFMNCSSCGVMNRRLIIVTLTETRDGQVLGRRC 339
QY 301 FEARICACGGRDRKADEDSIRKQVSDSTKNGDGTGRPFQNTHGQIOMTSIKKRSPDDE 360
DB 15 FEARICACGGRDRKADEDSIRKQVSDSTKNGDGTGRPFQNTHGQIOMTSIKKRSPDDE 399

RESULT 8
Q75922
ID Q75922 PRELIMINARY; PRT: 393 AA.
AC Q75922;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE P51 isoform DELNGAMMA (DN P63 gamma).
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Raghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075429; AAC62634.1; -
DR EMBL; AF116770; AAF43490.1; -
DR EMBL; AF116758; AAF43490.1; JOINED.
DR EMBL; AF116759; AAF43490.1; JOINED.
DR EMBL; AF116760; AAF43490.1; JOINED.
DR EMBL; AF116761; AAF43490.1; JOINED.
DR EMBL; AF116762; AAF43490.1; JOINED.
DR EMBL; AF116763; AAF43490.1; JOINED.
DR EMBL; AF116764; AAF43490.1; JOINED.
DR EMBL; AF116765; AAF43490.1; JOINED.
DR EMBL; AF124540; AAG45612.1; -
DR EMBL; AF124530; AAG45612.1; JOINED.
DR EMBL; AF124531; AAG45612.1; JOINED.
DR EMBL; AF124532; AAG45612.1; JOINED.
DR EMBL; AF124533; AAG45612.1; JOINED.
DR EMBL; AF124534; AAG45612.1; JOINED.
DR EMBL; AF124535; AAG45612.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 393 AA; 44658 MW; C6689B83FD701610 CRC64;

Query Match 84.6%; Score 379; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 129
DB 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
QY 130 TDYPGPHSFDVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTPPQGAIVRAM 189
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Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy      190 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 309
Db      195 PYEPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 254
Qy      310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRFRQNTHGQIOMTSIKKRRSPDDELLYLPVGR 369
Db      255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRFRQNTHGQIOMTSIKKRRSPDDELLYLPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPOHTIETIRYQQQQQHHLLQKLLSACFRNELVPRRTP 429
Db      315 EYEMLLKIKESLELMQYLPOHTIETIRYQQQQQHHLLQKLLSACFRNELVPRRTP 374
Qy      430 KOSDVFFRHSKPPNRSVYP 448
Db      375 KOSDVFFRHSKPPNRSVYP 393

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RESULT 9

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Q9P1B6
ID Q9P1B6 PRELIMINARY; PRT; 416 AA.
AC Q9P1B6;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE P51 isoform delNdelta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43493.1; JOINED.
DR EMBL; AF116758; AAF43493.1; JOINED.
DR EMBL; AF116759; AAF43493.1; JOINED.
DR EMBL; AF116760; AAF43493.1; JOINED.
DR EMBL; AF116761; AAF43493.1; JOINED.
DR EMBL; AF116762; AAF43493.1; JOINED.
DR EMBL; AF116763; AAF43493.1; JOINED.
DR EMBL; AF116764; AAF43493.1; JOINED.
DR EMBL; AF116765; AAF43493.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 416 AA; 46589 MW; A5974A14B25E3118 CRC64;

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Query Match 76.1%; Score 341; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      70 PoytNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db      15 PoytNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy      130 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134

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Qy      190 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 309
Db      195 PYEPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 254
Qy      310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRFRQNTHGQIOMTSIKKRRSPDDELLYLPVGR 369
Db      255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRFRQNTHGQIOMTSIKKRRSPDDELLYLPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPOHTIETIRYQQQQQHHLLQK 410
Db      315 EYEMLLKIKESLELMQYLPOHTIETIRYQQQQQHHLLQK 355

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RESULT 10

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Q9P1B5
ID Q9P1B5 PRELIMINARY; PRT; 461 AA.
AC Q9P1B5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE P51 isoform delNbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43492.1; JOINED.
DR EMBL; AF116758; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
DR EMBL; AF116763; AAF43492.1; JOINED.
DR EMBL; AF116764; AAF43492.1; JOINED.
DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;

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Query Match 76.1%; Score 341; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      70 PoytNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db      15 PoytNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy      130 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy      190 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 309

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Db 195 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPFRQNTGHGIQMTSIRKRRSPDDDELLYLPVGR 369
Db 255 GRDKADEDSIRKQVSDSTKNGDGTTRPPFRQNTGHGIQMTSIRKRRSPDDDELLYLPVGR 314
Qy 370 EYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQK 355

RESULT 11
Q9UP26 ID Q9UP26 PRELIMINARY; PRT; 461 AA.
AC Q9UP26;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang X., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Haglwa K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075433; AAC62638.1; -.
DR EMBL; AF124539; AAG45611.1; -.
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.
DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPATPSN 129
Db 15 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPATPSN 74
Qy 130 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy 250 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309
Db 195 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 195 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
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Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPFRQNTGHGIQMTSIRKRRSPDDDELLYLPVGR 369
Db 255 GRDKADEDSIRKQVSDSTKNGDGTTRPPFRQNTGHGIQMTSIRKRRSPDDDELLYLPVGR 314
Qy 370 EYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQK 355

RESULT 12
Q9P1B4 ID Q9P1B4 PRELIMINARY; PRT; 586 AA.
AC Q9P1B4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE P51 isoform delNalpa.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43491.1; -.
DR EMBL; AF116758; AAF43491.1; JOINED.
DR EMBL; AF116759; AAF43491.1; JOINED.
DR EMBL; AF116760; AAF43491.1; JOINED.
DR EMBL; AF116761; AAF43491.1; JOINED.
DR EMBL; AF116762; AAF43491.1; JOINED.
DR EMBL; AF116763; AAF43491.1; JOINED.
DR EMBL; AF116764; AAF43491.1; JOINED.
DR EMBL; AF116765; AAF43491.1; JOINED.
DR EMBL; AF116766; AAF43491.1; JOINED.
DR EMBL; AF116767; AAF43491.1; JOINED.
DR EMBL; AF116768; AAF43491.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPATPSN 129
Db 15 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPATPSN 74
Qy 130 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy 250 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309
Db 195 PYEPPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPFRQNTGHGIQMTSIRKRRSPDDDELLYLPVGR 369
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Db 255 GRDRKADEDSIRKQVSDSTKNGDCTKRPRQNTHTGIQMTSIKKRRSPDDDELLYLPVGR 314

QY 370 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQK 355

RESULT 13

Q9UBV9 ID Q9UBV9 PRELIMINARY; PRT; 586 AA.
AC Q9UBV9; MEDLINE-98448095; PubMed-9774969;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE DN P63 alpha.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
Dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
stomatitis: The CUSP autoantigen is a member of the p53 family.";
RL J. Invest. Dermatol. 0:0-0(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075431; AAC62636.1; -;
DR EMBL; AF091627; AAC43038.1; -;
DR EMBL; AF124539; AAG45610.1; -;
DR EMBL; AF124531; AAG45610.1; JOINED.
DR EMBL; AF124530; AAG45610.1; JOINED.
DR EMBL; AF124532; AAG45610.1; JOINED.
DR EMBL; AF124533; AAG45610.1; JOINED.
DR EMBL; AF124534; AAG45610.1; JOINED.
DR EMBL; AF124535; AAG45610.1; JOINED.
DR EMBL; AF124536; AAG45610.1; JOINED.
DR EMBL; AF124537; AAG45610.1; JOINED.
DR EMBL; AF124538; AAG45610.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1AF8629 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PONTNGLNMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSTFDALSPSPAFPSN 129

Db 15 PONTNGLNMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSTFDALSPSPAFPSN 74

QY 130 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189

Db 75 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134

QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVDEPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVDEPITGRQSVLV 194
QY 250 PYEPPQVGTETFTVLYNFMCMNSSCVGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 309
Db 195 PYEPPQVGTETFTVLYNFMCMNSSCVGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQVSDSTKNGDCTKRPRQNTHTGIQMTSIKKRRSPDDDELLYLPVGR 369
Db 255 GRDRKADEDSIRKQVSDSTKNGDCTKRPRQNTHTGIQMTSIKKRRSPDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQK 355

RESULT 14

O88897 ID O88897 PRELIMINARY; PRT; 483 AA.
AC O88897;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE TA*p63 gamma.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075434; AAC62639.1; -;
DR HSSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 63.4%; Score 284; DB 11; Length 483;
Best Local Similarity 100.0%; Pred. No. 7;le-290;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GATNKIELSMDCIRMQSDLSLSDPMPQYTNGLNMDQIQNGSSSTSPYNTDHAQNSV 104

Db 84 GATNKIELSMDCIRMQSDLSLSDPMPQYTNGLNMDQIQNGSSSTSPYNTDHAQNSV 143

QY 105 TAPSPYAQSSTFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 164

Db 144 TAPSPYAQSSTFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 203

QY 165 QIAKTCPIQIKVMTPPQGAIVRAMPYVKKAEHVTEVVKRCPNHLSREFNEGQIAPPSh 224

Db 204 QIAKTCPIQIKVMTPPQGAIVRAMPYVKKAEHVTEVVKRCPNHLSREFNEGQIAPPSh 263

QY 225 LIRVEGNSHAQYVDEPITGRQSVLVYPPEVQVGTETFTVLYNFMCMNSSCVGMNRRPILI 284

Db 264 LIRVEGNSHAQYVDEPITGRQSVLVYPPEVQVGTETFTVLYNFMCMNSSCVGMNRRPILI 323

QY 285 IVTLETRDQGVLRRCFEARICACPGDRKADEDSIRKQVSDS 328

Db 324 IVTLETRDQGVLRRCFEARICACPGDRKADEDSIRKQVSDS 367

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RESULT 15
Q9QWZ0
AC Q9QWZ0 PRELIMINARY; PRT; 555 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TA*p63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., Mckeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075435; AAC62640.1; -.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB8987 CRC64;

Query Match 63.4%; Score 284; DB 11; Length 555;
Best Local Similarity 100.0%; Pred. No. 8e-290;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GATNKEISMDCIRMQDSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSV 104
Db 84 GATNKEISMDCIRMQDSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSV 143
Qy 105 TAPSPYAQPSTFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 164
Db 144 TAPSPYAQPSTFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 203
Qy 165 QIAKTCPIQIKVMTPPQGAIVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSH 224
Db 204 QIAKTCPIQIKVMTPPQGAIVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSH 263
Qy 225 LIRVEGNSHAQYVEDPITGRQSVLVYPYEPQVGTEFTVLYNFMCSNCSVGGMNRRLI 284
Db 264 LIRVEGNSHAQYVEDPITGRQSVLVYPYEPQVGTEFTVLYNFMCSNCSVGGMNRRLI 323
Qy 285 IVTLETRDGVIGRRCFEARICACPGDRKADEDSIRKQVSDS 328
Db 324 IVTLETRDGVIGRRCFEARICACPGDRKADEDSIRKQVSDS 367
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Search completed: June 24, 2003, 22:25:04
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:19:31 ; Search time 15 Seconds
(without alignments)
1238.760 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 448

Sequence: 1 MSQSTQTNEFLSPEVFOHIW.....PKQSDVFRHSPKPNRSVYP 448

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 segs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	4.9	636	1 P73_HUMAN	O15350 homo sapien
2	22	4.9	637	1 P73_CERAE	Q9XSK8 cercopithec
3	15	3.3	369	1 P53_BARBU	Q9W678 barbus barb
4	13	2.9	367	1 P53_CHICK	P10360 gallus gall
5	13	2.9	396	1 P53_ONCMY	P25035 oncorhynchu
6	11	2.5	352	1 P53_ORYLA	P79820 oryzias lat
7	10	2.2	393	1 P53_CRIGR	Q09185 cricetus
8	10	2.2	393	1 P53_TUPGB	Q9TCA1 tupaia glis
9	10	2.2	396	1 P53_MESAU	Q00366 mesocricetu
10	9	2.0	195	1 HUNB_DRODA	O46262 drosophila
11	9	2.0	196	1 HUNB_DROAA	O46234 drosophila
12	9	2.0	201	1 AST5_DROME	P10083 drosophila
13	9	2.0	207	1 P53_EQUAS	Q29480 equus asinu
14	9	2.0	280	1 P53_HORSE	P79892 equus cabal
15	9	2.0	314	1 P53_SPEBE	O64662 spermophilu
16	9	2.0	342	1 P53_XIPHE	O57538 xiphophorus
17	9	2.0	342	1 P53_XIPMA	Q92143 xiphophorus
18	9	2.0	363	1 P53_XENLA	P07193 xenopus lae
19	9	2.0	366	1 P53_PLAFE	O12946 platichthys
20	9	2.0	367	1 P53_TETMU	Q9W679 tetraodon m
21	9	2.0	373	1 P53_BRARE	P79734 brachydanio
22	9	2.0	376	1 P53_ICTPU	Q93379 ictalurus p
23	9	2.0	381	1 P53_CANFA	Q29537 canis famil
24	9	2.0	382	1 P53_SHEEP	P51664 ovis aries
25	9	2.0	386	1 P53_BOVIN	Q29628 bos taurus
26	9	2.0	386	1 P53_FELCA	P41685 felis silve
27	9	2.0	386	1 P53_PIG	Q9TUB2 sus scrofa
28	9	2.0	390	1 P53_MOUSE	P02340 mus musculu
29	9	2.0	391	1 P53_CAVPO	Q9WUR6 cavla porce
30	9	2.0	391	1 P53_MARMO	O36006 marmota mon
31	9	2.0	391	1 P53_RABIT	Q95330 oryctolagus
32	9	2.0	391	1 P53_RAT	P10361 rattus norv
33	9	2.0	393	1 P53_CERAE	P13481 cercopithec

RESULT 1

P73_HUMAN
ID P73_HUMAN STANDARD; PRT; 636 AA.
AC O15350; O15351; Q9NTRK8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related
DE protein).
GN TP73 OR P73.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE-Colon;
RX MEDLINE=97433090; PubMed=9288759;
RA Raghav M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,
RA Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,
RA Caput D.;
RT "Monoclonally expressed gene related to p53 at 1p36, a region
RT frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=99289209; PubMed=10362363;
RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K.,
RA Harris C.C.;
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";
RN Oncogene 18:3415-3421(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98389621; PubMed=9721206;
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,
RA Jenkins R., Smith D.I., Liu W.;
RT "Genomic organization and mutation analysis of p73 in
RT oligodendrogliomas with chromosome 1 p-arm deletions.";
RN Genomics 51:359-363(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).
RC TISSUE=Neuroblastoma;
RX MEDLINE=99021697; PubMed=9802988;
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,
RA Annicchiarico-Petruzzelli M., Leviero M., Melino G.;
RT "Two new p73 splice variants, gamma and delta, with different
RT transcriptional activity.";
RL J. Exp. Med. 188:1763-1768(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
RC TISSUE=Lymphocytes, Breast Cancer, Hepatoma, and Skin;
RX MEDLINE=99310938; PubMed=10381648;
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,
RA Costanzo A., Leviero M., Knight R.A.;
RT "Additional complexity in p73: induction by mitogens in lymphoid cells
RT and identification of two new splice variants epsilon and zeta.";

34 9 2.0 393 1 P53_HUMAN P04637 homo sapien
35 9 2.0 393 1 P53_MACFA P56423 macaca fasc
36 9 2.0 393 1 P53_MACMU P56424 macaca mula
37 9 2.0 481 1 KNIR_DROVI Q24753 drosophila
38 9 2.0 635 1 HMLA_DROME P10105 drosophila
39 9 2.0 816 1 ATX1_HUMAN P54253 homo sapien
40 9 2.0 1167 1 WCL_NEUCR Q01371 neurospora
41 9 2.0 1394 1 E75B_DROME P17672 drosophila
42 8 1.8 54 1 SASG_BACFI P35142 bacillus fi
43 8 1.8 150 1 CKS1_YEAST P20486 saccharomyc
44 8 1.8 170 1 VIM1_CARAU P48671 carassius a
45 8 1.8 192 1 HUNB_DROAD O46232 drosophila

ALIGNMENTS

Cell Death Differ. 6:389-390(1999).
[6] SEQUENCE FROM N.A. (ISOFORM KAPPA).
RA Thomas D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
RX MEDLINE-99318135; PubMed-10391251;
RA Kharbada S., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
to DNA damage";
RL Nature 399:814-817(1999).
RN [8]
RP ERRATUM.
RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RL Kharbada S., Weichselbaum R., Kufe D.;
RN Nature 400:792-792(1999).
[9]
RP FUNCTION.
RX MEDLINE-99217940; PubMed-10203277;
RA Kaelin W.G. Jr.;
RT "The emerging p53 gene family";
RL J. Natl. Cancer Inst. 91:594-598(1999).
RN [10]
RP STRUCTURE BY NMR OF 439-506.
RX MEDLINE-99380160; PubMed-10449409;
RA Chi S.W., Ayed A., Arrowsmith C.H.;
RT "Solution structure of a conserved C-terminal domain of p73 with
structural homology to the SAM domain";
RL EMBO J. 18:4438-4445(1999).
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC PROTEIN.
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 7 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA,
CC DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS
CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE
CC SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME
CC TO THE ALPHA ISOFORM.
CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN. A CENTRAL DNA
CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL; Y11416; CAAT72220.1; -
DR EMBL; Y11416; CAAT72221.1; -
DR EMBL; Y11416; CAAT72219.1; -
DR EMBL; AF077628; AAC61887.1; -
DR EMBL; AF077616; AAC61887.1; JOINED.
DR EMBL; AF077617; AAC61887.1; JOINED.

DR EMBL; AF077618; AAC61887.1; JOINED.
DR EMBL; AF077619; AAC61887.1; JOINED.
DR EMBL; AF077620; AAC61887.1; JOINED.
DR EMBL; AF077621; AAC61887.1; JOINED.
DR EMBL; AF077622; AAC61887.1; JOINED.
DR EMBL; AF077623; AAC61887.1; JOINED.
DR EMBL; AF077624; AAC61887.1; JOINED.
DR EMBL; AF077625; AAC61887.1; JOINED.
DR EMBL; AF077626; AAC61887.1; JOINED.
DR EMBL; AF077627; AAC61887.1; JOINED.
DR EMBL; AF079094; AAC61887.1; JOINED.
DR EMBL; AF079082; AAC61887.1; JOINED.
DR EMBL; AF079083; AAC61887.1; JOINED.
DR EMBL; AF079084; AAC61887.1; JOINED.
DR EMBL; AF079085; AAC61887.1; JOINED.
DR EMBL; AF079086; AAC61887.1; JOINED.
DR EMBL; AF079087; AAC61887.1; JOINED.
DR EMBL; AF079088; AAC61887.1; JOINED.
DR EMBL; AF079089; AAC61887.1; JOINED.
DR EMBL; AF079090; AAC61887.1; JOINED.
DR EMBL; AF079091; AAC61887.1; JOINED.
DR EMBL; AF079092; AAC61887.1; JOINED.
DR EMBL; AF079093; AAC61887.1; JOINED.
DR EMBL; ALI36528; CAB92742.1; -
DR PDB; 1COK; 17-AUG-99.
DR TRANSFAC; T04931; -
DR Genew; HGNC:12003; TP73.
DR MIM; 601990; -
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
KW 3D-structure. 1 46
FT DOMAIN 1 55
FT DOMAIN 287 304
FT DOMAIN 346 435
FT DOMAIN 168 171
FT DOMAIN 391 394
FT DOMAIN 483 486
FT DOMAIN 131 310
FT MOD_RES 99 99
FT VARSPLIC 282 282
FT VARSPLIC 495 636
FT VARSPLIC 400 476
FT VARSPLIC 477 636
FT VARSPLIC 400 403
FT VARSPLIC 404 636
FT VARSPLIC 400 445
FT VARSPLIC 446 526
FT VARSPLIC 400 495
SQ SEQUENCE 636 AA; 69623 MW; A467493C5D93EE0 CRC64;
Query Match 4.9%; Score 22; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 5,2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 LYFMCNCSGVGMNRRPILII 285

Db 253 LYNECMSSCVGMNRRPILII 274
|||||

RESULT 2

P73_CERAE STANDARD; PRT; 637 AA.
AC Q9XSK8; Q9TSQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
GN TP73 OR P73.
OS Cercopithecus aethiops (Green monkey) (Grivet).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL; Y11419; CAA72224.1; -;
DR EMBL; Y11419; CAA72225.1; -;
DR HSSP; O15350; ICKK.
DR InterPro; IPR002117; P53.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
FT VARSPPLIC 495 637 SFLTGLGCPNCIEFTSGOQSIVHLQNLTIEDLGALKIPE QYRMTIWRGLQDLKQGHYDGAQAQLRSSNAIAISIGGSG ELQQRVMEAVHFRVHTITIPNRGGPGAGDEWADFGL PDCRKARKPIKEEFTAEIHF -> RTWGP (IN ISOFORM BETA)
SQ SEQUENCE 637 AA; 69630 MW; 7CB200B919C9C70A CRC64;

Query Match 4.9%; Score 22; DB 1; Length 637;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 LYNECMSSCVGMNRRPILII 285
|||||

Db 253 LYNECMSSCVGMNRRPILII 274

RESULT 3

P53_BARBU STANDARD; PRT; 369 AA.
AC Q9W678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RC "Evolutionary conservancy of p53 gene sequences in fish."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL; AF071570; AAD34212.1; -;
DR HSSP; P04637; ITUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 66 256 BY SIMILARITY.
FT DOMAIN 298 329 OLIGOMERIZATION.
FT DOMAIN 342 369 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;

Query Match 3.3%; Score 15; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 EFTTVLYNFMNCSSC 273
|||||
Db 192 EFTTVLYNFMNCSSC 206
|||||

RESULT 4

P53_CHICK STANDARD; PRT; 367 AA.
ID P53_CHICK
AC P10360;

DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAFAS;
 RX MEDLINE=89083584; PubMed=3060861;
 RA Soussi T.;
 RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
 oncoprotein.";
 RL Nucleic Acids Res. 16:11383-11383(1988).
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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 DR EMBL; X13057; CAA31456.1; -
 DR PIR; S02193; S02193.
 DR HSSP; P04637; ITUP.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 87 278 BY SIMILARITY.
 FT DOMAIN 308 339 OLIGOMERIZATION.
 FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 367 AA; 40169 MW; FC37D0FCDF9195B6 CRC64;
 Query Match 2.9%; Score 13; DB 1; Length 367;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 261 TTVLYNFCMNCSSC 273
 Db 216 TTVLYNFCMNCSSC 228
 RESULT 5
 P53_ONCMY STANDARD; PRT; 396 AA.
 ID P53_ONCMY
 AC P25035;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OC NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92210006; PubMed=1339362;
 RA de Fromental C.C.; Padkel F.; Chapus A.; Baney C.; May P.; Soussi T.;
 RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";
 RL Gene 112:241-245(1992).
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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 DR EMBL; M75145; AAA49605.1; -
 DR PIR; JH0631; JH0631.
 DR HSSP; P04637; ITUP.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 90 281 BY SIMILARITY.
 FT DOMAIN 325 356 OLIGOMERIZATION.
 FT DOMAIN 369 392 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;
 Query Match 2.9%; Score 13; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 261 TTVLYNFCMNCSSC 273
 Db 219 TTVLYNFCMNCSSC 231
 RESULT 6
 P53_ORYLA STANDARD; PRT; 352 AA.
 ID P53_ORYLA
 AC P79820; Q9PSU7; Q9PSU8;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 CC Nebiiformes; Adrianchthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=97305153; PubMed=9161419;
 RX Krause M.K., Rhodes L.D., van Beneden R.J.;
 RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka
 RT (Oryzias latipes) and evaluation of mutational hotspots in MNG-
 RT exposed fish";
 RL Gene 189:101-106(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT THR-91.
 RC STRAIN=Himedaka;
 RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
 RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the
 RT Japanese Medaka (Oryzias latipes).";
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation
 CC as a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC
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 CC
 CC EMBL: U57306; AAC60146.1; -;
 CC EMBL: AF003949; AAD01195.1; -;
 CC EMBL: AF003950; AAD01196.1; -;
 CC HSSP: P04637; 1YCS.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PRODOM: P0002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
 FT DOMAIN 1 48
 FT DNA_BIND 87 273
 FT DOMAIN 302 331
 FT DOMAIN 334 350
 FT DOMAIN 283 295
 FT MOD_RES 351 351
 FT VARIANT 91 91
 FT CONFLICT 22 22 MISSING (IN REF. 1).
 SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;
 Query Match 2.5%; Score 11; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 304 RICACPGDRK 314
 DB 254 RICACPGDRK 264
 RESULT 7
 P53_CRIGR
 ID P53_CRIGR STANDARD; PRT; 393 AA.

AC 009185; Q64397; P97258; P97788;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chaung W., Mi L.J., Boorstein R.J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97183659; PubMed=9031625;
 RA Lee H., Lerner J.M., Hamlin J.L.;
 RT "Cloning and characterization of Chinese hamster p53 cDNA.";
 RL Gene 184:177-183(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic fibroblast;
 RA Shimizu T., Nikaudo O., Suzuki F.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC
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 CC
 CC EMBL: Y08900; CAA70108.1; -;
 CC EMBL: Y08901; CAA70109.1; -;
 CC EMBL: U50395; AAC53040.1; -;
 CC EMBL: D86070; BAAL3004.1; -;
 CC HSSP: P04637; 1TUP.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PRODOM: P0002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 45
 FT DNA_BIND 102 292
 FT DOMAIN 325 356
 FT DOMAIN 368 387
 FT DOMAIN 311 323
 FT MOD_RES 392 392
 FT VARIANT 133 133
 FT VARIANT 135 135
 FT CONFLICT 103 103
 FT CONFLICT 103 103 Y -> F (IN REF. 2).
 SQ SEQUENCE 393 AA; 43378 MW; 2A7830E788311689 CRC64;

Query Match

Best Local Similarity 2.2%; Score 10; DB 1; Length 393;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313
Db 273 RICACPGDR 282

RESULT 8

ID P53_TUPGB STANDARD; PRT; 393 AA.
AC O9TAL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR p53.
OS Tupala gliis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupala.
OX NCBI_TaxID=9396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chinensis; TISSUE=Liver;
RA Park U., Lee Y.;
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL "Wild-type p53 sequence of tree shrews.";
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; AF175893; AAF22640.1; --
DR HSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 102 292 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;

Query Match

Best Local Similarity 2.2%; Score 10; DB 1; Length 393;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313
Db 273 RICACPGDR 282

RESULT 9

ID P53_MESAU STANDARD; PRT; 396 AA.
AC Q00366; P97276;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian; TISSUE=Kidney;
RA MEDLINE=92210007; PubMed=1555773;
RA Legros Y., McIntyre P., Soussi T.;
RT "The cDNA cloning and immunological characterization of hamster p53.";
RL Gene 112:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Hou E.W., Wiseman R.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; M75144; AAB37085.1; --
DR EMBL; U07182; AAB41344.1; --
DR PIR; JH0633; JH0633.
DR HSP; P04637; ITUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 105 295 BY SIMILARITY.
FT DOMAIN 328 359 OLIGOMERIZATION.
FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 186 188 G -> S (IN REF. 2).

SQ SEQUENCE 396 AA; 43631 MW; 906EF02568099BE3 CRC64;

Query Match 2.2%; Score 10; DB 1; Length 396;

Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313

|||||

Db 276 RICACPGDR 285

RESULT 10

HUNB_DRODA

ID HUNB_DRODA STANDARD; PRT; 195 AA.

AC 046263;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Hunchback protein (Fragments).

GN HB.

OS Drosophila dasycnemia (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=58308;

[1]

RP SEQUENCE FROM N.A.

RA Baker R.H., Desalle R.;

RT "Multiple sources of character information and the phylogeny of

RT Hawaiian drosophilids."

RL Syst. Biol. 46:654-673(1997).

CC -1- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT

CC OF HEAD STRUCTURES (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.

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DR EMBL; U93026; AAC03274.1; -.

DR EMBL; U93027; AAC03275.1; -.

DR FlyBase; FBgn0024069; Ddaa\hb.

KW Developmental protein; Gap protein; Zinc-finger;

KW Metal-binding; DNA-binding; Repeat; Nuclear protein.

FT NON_TER 1

FT DOMAIN 17 29 POLY-HIS.

FT NON_CONS 66 81 POLY-GLN.

FT NON_TER 102 103

FT DOMAIN 130 136 POLY-ALA.

FT NON_TER 195 195

SQ SEQUENCE 195 AA; 21335 MW; 4DA02122E1532AC3 CRC64;

Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 195;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 QQQQQQHGH 406

|||||

Db 68 QQQQQQHGH 76

RESULT 11

HUNB_DROAA

ID HUNB_DROAA STANDARD; PRT; 196 AA.

AC 046234; 046235;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hunchback protein (Fragments).

GN HB.

OS Drosophila adunca (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=46893;

[1]

RP SEQUENCE FROM N.A.

RA Baker R.H., Desalle R.;

RT "Multiple sources of character information and the phylogeny of

RT Hawaiian Drosophilids."

RL Syst. Biol. 46:654-673(1997).

CC -1- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT

CC OF HEAD STRUCTURES (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U92998; AAC03247.1; -.

DR EMBL; U92999; AAC03246.1; -.

DR FlyBase; FBgn0024132; Dadu\hb.

KW Developmental protein; Gap protein; Zinc-finger;

KW Metal-binding; DNA-binding; Repeat; Nuclear protein.

FT NON_TER 1

FT DOMAIN 17 29 POLY-HIS.

FT NON_CONS 65 80 POLY-GLN.

FT NON_TER 101 102

FT NON_TER 196 196

SQ SEQUENCE 196 AA; 21683 MW; F961D7184FFE4C6F CRC64;

Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 196;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 QQQQQQHGH 406

|||||

Db 67 QQQQQQHGH 75

RESULT 12

AST5_DROME

ID AST5_DROME STANDARD; PRT; 201 AA.

AC P10083; Q9W5G4;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Achaete-scute complex protein T5 (Achaete).

GN AC OR T5 OR EG:125H10.3 OR CG3796.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-Canton-S;

RX MEDLINE=87273503; PubMed=3111716;

RA Villares R., Cabrera C.V.;

RT "The achaete-scute gene complex of D. melanogaster: conserved domains

RT in a subset of genes required for neurogenesis and their homology to

RT myc."

RL Cell 50:415-424(1987).

RN [2]

SEQUENCE FROM N.A.
 RC MEDLINE-20196011; PubMed-10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
 RA Minano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
 RA Papagiannakis G., Spanos L., Cox S., Siden-Klamos E., Bolshakov S.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamskou N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 "From sequence to chromosome: the tip of the x chromosome of D.
 melanogaster";
 Science 287:2220-2222(2000).
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nalato D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*";
 Science 287:2185-2195(2000).
 -1- FUNCTION: AS-C PROTEINS ARE INVOLVED IN THE DETERMINATION OF THE
 NEURONAL PRECURSORS IN THE PERIPHERAL NERVOUS SYSTEM AND THE
 CENTRAL NERVOUS SYSTEM.
 CC SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN.
 CC TISSUE SPECIFICITY: L(1)SC, SC AND AC STRONGLY LABEL THE
 CC PRESUMPTIVE STOMATOGASTRIC NERVOUS SYSTEM, WHILE ASE IS MORE
 CC PROMINENT IN THE PRESUMPTIVE PROCEPHALIC LOBE.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
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 CC -----
 CC EMBL; M17120; AAA28312.1; -
 CC EMBL; AL023873; CAA19641.1; -
 CC EMBL; AE003417; AAF45498.1; -
 CC PIR; A43731; A43731.
 CC TRANSFAC; T00005; -
 CC FlyBase; FBgn0000022; ac.
 CC InterPro; IPR001092; HLH_basic.
 CC Pfam; PF00010; HLH; 1.
 CC SMART; SM00353; HLH; 1.
 CC PROSITE; PS00038; HLH_1; 1.
 CC PROSITE; PS00888; HLH_2; 1.
 CC Neurogenesis; Differentiation; Developmental protein; DNA-binding.
 CC DNA_BIND 27 37
 CC DOMAIN 38 91
 CC SEQUENCE 201 AA; 22753 MW; AAA90600CA764C0 CRC64;
 CC
 CC Query Match 2.0%; Score 9; DB 1; Length 201;
 CC Best Local Similarity 100.0%; Pred. No. 0.24;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 399 QQQQQHQL 407
 CC Db 115 QQQQQHQL 123
 CC
 CC RESULT 13
 CC P53_EQUAS
 CC ID P53_EQUAS STANDARD; PRT; 207 AA.
 CC AC Q29480;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).
 CC GN TP53.
 CC OS Equus asinus (Donkey).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CC OX NCBI_Taxid:9793;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE-96342529; PubMed-8746464;
 CC RA Nasir L., Reid S.W.;
 CC "Nucleotide sequence of exons 5 to 9 of the p53 tumour-suppressor
 CC gene of the donkey (*Equus asinus*).";
 CC RL DNA Seq. 6:61-63(1995).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- CELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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DR EMBL; U26741; AAB41265.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT NON_TER 1
FT DNA_BIND <1 168
FT DOMAIN 201 >207 BY SIMILARITY.
FT DOMAIN 187 199 OLIGOMERIZATION.
FT NON_TER 207
SQ SEQUENCE 207 AA; 23428 MW; 973EBD85910B498E CRC64;

Query Match 2.0%; Score 9; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 265 YNFMNCSSC 273
Db 110 YNFMNCSSC 118
|||||

RESULT 14
P53_HORSE STANDARD; PRT; 280 AA.
AC P79892; Q29481;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).
GN TP53 OR P53.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE OF 1-263 FROM N.A.
RC TISSUE-Spleen;
RX MEDLINE=97070350; PubMed=8913276;
RA Pazzi K.A., Kraegel S.A., Griffey S.M., Theon A.P., Madewell B.R.;
RT "Analysis of the equine tumor suppressor gene p53 in the normal horse
and in eight cutaneous squamous cell carcinomas.";
RL Cancer Lett. 107:125-130(1996).
RN [2]
RP SEQUENCE OF 76-280 FROM N.A.
RX MEDLINE=96293865; PubMed=8722575;
RA Nasir L., Reid S.W.;
RT "Nucleotide sequence of exons 5 to 9 of the p53 tumour-suppressor
gene of the horse (Equus caballus).";
RL DNA Seq. 6:185-187(1996).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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or send an email to license@isb-sib.ch).
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DR EMBL; S83123; AAB46899.1; -.
DR EMBL; U37120; AAB18936.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT NON_TER 1
FT DNA_BIND 52 243 BY SIMILARITY.
FT DOMAIN 276 >280 OLIGOMERIZATION.
FT DOMAIN 262 274 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT CONFLICT 79 79 T -> A (IN REF. 2).
FT CONFLICT 83 83 L -> M (IN REF. 2).
FT CONFLICT 111 111 A -> V (IN REF. 2).
FT CONFLICT 138 138 G -> A (IN REF. 2).
FT NON_TER 280
SQ SEQUENCE 280 AA; 30985 MW; 040F12030B5ACEE9 CRC64;

Query Match 2.0%; Score 9; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 265 YNFMNCSSC 273
Db 185 YNFMNCSSC 193
|||||

RESULT 15
P53_SPEBE STANDARD; PRT; 314 AA.
AC Q64662;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).
GN TP53.
OS Spomophilus beecheyi (Beechey ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spomophilus.
OX NCBI_TaxID=34862;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Thymus;
RX MEDLINE=95007566; PubMed=7923176;
RA Rivkina M.B., Cullen J.M., Robinson W.S., Marlon P.L.;
RT "State of the p53 gene in hepatocellular carcinomas of ground
squirrels and woodchucks with past and ongoing infection with
hepadnaviruses.";
RL Cancer Res. 54:5430-5437(1994).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----

DR EMBL; U43902; AA85628.1; -
 DR HSP; P04637; LYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR ProDom; PD002681; P53; 1.
 DR ProSITE; PS00348; P53; 1.
 KW Anti-Oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT NON_TER 1
 FT DOMAIN <1 24 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 80 270 BY SIMILARITY.
 FT DOMAIN 303 >314 OLIGOMERIZATION.
 FT DOMAIN 289 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT NON_TER 314 314
 SQ SEQUENCE 314 AA; 34618 MW; 4F949656A8BED1F6 CRC64;

Query Match
 Best Local Similarity 2.0%; Score 9; DB 1; Length 314;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 GGMNRRPIL 283
 Db 222 GGMNRRPIL 230
 |||||

Search completed: June 24, 2003, 22:26:09
 Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2003, 22:25:12 ; Search time 19 Seconds
(without alignments)
2266.748 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 448

Sequence: 1 MSQSTQNEFLSPVFOHIW.....PKQSDVFRHKKPPNRSVYP 448

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	2.9	367	1 S02193	cellular tumor ant
2	13	2.9	396	1 JH0631	cellular tumor ant
3	10	2.2	393	2 JC6176	tumor suppressor p
4	10	2.2	396	1 JH0633	cellular tumor ant
5	9	2.0	201	2 A43731	Achaete-scute comp
6	9	2.0	363	1 A29376	cellular tumor ant
7	9	2.0	381	2 S38824	cellular tumor ant
8	9	2.0	386	1 S51648	cellular tumor ant
9	9	2.0	390	1 DNWS53	cellular tumor ant
10	9	2.0	391	1 S02192	cellular tumor ant
11	9	2.0	391	2 JC6193	tumor suppressor p
12	9	2.0	393	1 DNH053	cellular tumor ant
13	9	2.0	393	1 S06594	cellular tumor ant
14	9	2.0	481	2 A56346	transcription fact
15	9	2.0	629	2 A30168	homeotic protein L
16	9	2.0	635	2 S01184	homeotic protein L
17	9	2.0	638	1 A30350	dorsal protein - f
18	9	2.0	816	2 S46268	ataxin-1 - human
19	9	2.0	1062	2 G86325	hypothetical prote
20	9	2.0	1094	2 S49313	protein kinase - s
21	9	2.0	1145	2 T18235	transcription acti
22	9	2.0	1154	2 S9206	regulator protein
23	9	2.0	1394	2 B34598	ecdysone-induced p
24	9	2.0	1893	2 A56158	eye development pr
25	8	1.8	54	2 JU0155	spore protein gamm
26	8	1.8	77	2 I46226	cellular tumor ant
27	8	1.8	107	2 T25670	hypothetical prote
28	8	1.8	150	1 OKBYS1	cell division cont
29	8	1.8	158	2 F84776	probable RAV2-like

30	8	1.8	170	2 I50482	vimentin A1 - gold
31	8	1.8	173	2 A47303	FT2-F1 steroid rec
32	8	1.8	191	2 S35570	sex-determining pr
33	8	1.8	201	2 S23324	gene achaeete prote
34	8	1.8	215	1 S61138	hypothetical prote
35	8	1.8	224	2 D46177	enhancer of split
36	8	1.8	230	2 T49555	related to high cy
37	8	1.8	243	2 T24981	hypothetical prote
38	8	1.8	255	2 A60637	merozoite antigen
39	8	1.8	264	1 WMTMCV	30K protein - cucu
40	8	1.8	264	1 WMTMSH	29K protein - cucu
41	8	1.8	265	2 A48121	retrovirus-related
42	8	1.8	267	1 S30863	BMH1 protein - yea
43	8	1.8	301	2 JW0079	heterogeneous nucl
44	8	1.8	330	2 A35915	homeotic protein A
45	8	1.8	390	1 B49070	ecdysone-inducible

ALIGNMENTS

RESULT 1

S02193
cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02193
R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584; PMID:3060861
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <S0>
C:Cross-references: EMBL:X13057; NID:G63740; PIDN:CAA31456.1; PID:G63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
F:161,164,224,228/Binding site: zinc (Cys, His, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.9%; Score 13; DB 1; Length 367;

Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TTVLYNFMNCSSC 273

Db 216 TTVLYNFMNCSSC 228

RESULT 2

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:M75145; NID:G213828; PIDN:AAA49605.1; PID:G213829
A:Experimental source: liver
C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.9%; Score 13; DB 1; Length 396;

Best Local Similarity 100.0%; Pred. No. 6.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TTLYNFMNCSSC 273
 |||||
 Db 219 TTLYNFMNCSSC 231

RESULT 3

JC6176

tumor suppressor protein p53 - Chinese hamster

C:Species: Cricetulus griseus (Chinese hamster)

C:Date: 11-Apr-1997 #sequence_revision 09-May-1999

C:Accession: JC6176 #text_change 23-Jul-1999

R:Lee, H.; Larner, J.M.; Hamlin, J.L.

Gene 184, 177-183, 1997

A:Title: Cloning and characterization of Chinese hamster p53 cDNA.

A:Reference number: JC6176; MUID:97183659; PMID:9031625

A:Contents: liver

A:Accession: JC6176

A:Molecule type: mRNA

A:Residues: 1-393 <LEE>

A:CROSS-references: GB:U50395; NID:g1842229; PIDN:AA53040.1; PID:g1842230

C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage

C:Genetics: recombination by protein/protein interactions.

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: liver; tumor

Query Match

Best Local Similarity 2.2%; Score 10; DB 2; Length 393;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313

|||

Db 273 RICACPGDR 282

RESULT 4

JH0633

cellular tumor antigen p53 - golden hamster

N:Alternate names: tumor-suppressor protein p53

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999

C:Accession: JH0633 #text_change 10-Sep-1999

R:Legros, Y.; McIntyre, P.; Soussi, T.

Gene 112, 247-250, 1992

A:Title: The cDNA cloning and immunological characterization of hamster p53.

A:Reference number: JH0633; MUID:92210007; PMID:1555773

A:Accession: JH0633

A:Molecule type: mRNA

A:Residues: 1-396 <LEG>

A:CROSS-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415

A:Experimental source: Kidney, strain MP1

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph

F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 2.2%; Score 10; DB 1; Length 396;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313

|||

Db 276 RICACPGDR 285

RESULT 5

A43731

Achaete-scute complex protein T5 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 21-Jul-2000
 C:Accession: A43731
 R:Villares, R.; Cabrera, C.V.
 Cell 50, 415-424, 1987

A:Title: The achaete-scute gene complex of Drosophila melanogaster: conserved domains

A:Reference number: A43731; MUID:87273503; PMID:3111716

A:Accession: A43731

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-201 <VIL>

A:CROSS-references: GB:M17120; NID:g156744; PIDN:AAA28312.1; PID:g156747

C:Genetics:

A:Gene: FlyBase:ac

A:CROSS-references: FlyBase:FBgn0000022

C:Keywords: DNA binding

Query Match

Best Local Similarity 2.0%; Score 9; DB 2; Length 201;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 QQQQQHQHLL 407

|||||

Db 115 QQQQQHQHLL 123

RESULT 6

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999

C:Accession: A29376; S61531; S72313; I51639

R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a prot

A:Reference number: A29376; MUID:88143684; PMID:2830576

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SOU>

A:CROSS-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopu

A:Reference number: I51639; MUID:94134403; PMID:8302570

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293,295-363 <HOE>

A:CROSS-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.

submitted to the EMBL Data Library, March 1994

A:Reference number: S72313

A:Accession: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOE>

A:CROSS-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F:150,153,213,217/Binding site: zinc (Cys, His, Cys) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 363;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283

|||||

Db 219 GGMNRRPIL 227

RESULT 7

S38824

cellular tumor antigen p53, minor splice form - mouse

C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38824; S35478
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640; PMID:3023970
A:Accession: S38824
A:Molecule type: mRNA
A:Residues: 1-381 <ARA>
A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
R:Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tissues
A:Reference number: S35478; MUID:92253421; PMID:1579500
A:Accession: S35478
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-381 <HNA>
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks the 5' not known.

C:Superfamily: cellular tumor antigen p53
C:Keywords: alternative splicing; phosphoprotein; zinc
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7-9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 2.0%; Score 9; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283
|||||
DB 241 GGMNRRPIL 249

RESULT 8

S51648 cellular tumor antigen p53 - bovine

N:Alternate names: tumor-suppressor protein p53
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S51648
R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.
Submitted to the EMBL Data Library, September 1994
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its genomic organization
A:Reference number: S51648
A:Accession: S51648
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-386 <DEQ>
A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0%; Score 9; DB 1; Length 386;

Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 YNFCNSSC 273
|||||
DB 227 YNFCNSSC 235

RESULT 9

DNMS53 cellular tumor antigen p53 - mouse

N:Alternate names: oncoprotein p53
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C:Accession: A22739; S06336; A02684; S38822; S40014; I48703
R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A:Reference number: A22739; MUID:85027173; PMID:6092064
A:Accession: A22739
A:Molecule type: DNA
A:Residues: 1-134, 'V', 136-390 <BIE>
A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;
R:Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A:Reference number: S06336; MUID:88221682; PMID:3329909
A:Accession: S06336
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-134, 'V', 136-390 <CHU>
R:Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
A:Reference number: A02684; MUID:84068204; PMID:6646235
A:Accession: A02684
A:Molecule type: mRNA
A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>
A:Cross-references: GB:X01237; GB:K01700; NID:g53575
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640; PMID:3023970
A:Accession: S38822
A:Molecule type: mRNA
A:Residues: 1-390 <ARA1>
A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
A:Accession: S38823
A:Molecule type: mRNA
A:Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Submitted to the EMBL Data Library, July 1988
A:Reference number: S40014
A:Accession: S40014
A:Molecule type: mRNA
A:Residues: 1-167, 'G', 169-390 <ARA3>
A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201
R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding
A:Reference number: I48703; MUID:84272240; PMID:6379601
A:Accession: I48703
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>
A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
C:Comment: This DNA-binding protein plays an essential role in the regulation of cell
C:Superfamily: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: L2 loop
 F:168-178/Region: conserved region III
 F:231-252/Region: conserved region IV
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
 F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0% Score 9; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 GGMNRRPIL 283
 Db 241 GGMNRRPIL 249
 |||||

RESULT 10

S02192
 Cellular tumor antigen p53 - rat
 N:Alternate names: gene p53 protein; nuclear oncoprotein p53
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S02192; S41149
 R:Sousai, T.; de Fromental, C.C.; Breugnot, C.; May, E.
 Nucleic Acids Res. 16, 11384, 1988
 A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
 A:Reference number: S02192; MUID:89083585; PMID:3060862
 A:Accession: S02192
 A:Molecule type: mRNA
 A:Residues: 1-391 <SOU>
 A:Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829
 R:Hulla, J.E.; Schneider, R.P.
 Nucleic Acids Res. 21, 713-717, 1993
 A:Title: Structure of the rat p53 tumor suppressor gene.
 A:Reference number: S41149; MUID:93181268; PMID:8441680
 A:Accession: S41149
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-173, 'W', 175-391 <HUL>
 A:Cross-references: EMBL:L07909
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
 C:Genetics:
 A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
 F:174,177,236,240/Binding site: zinc (Cys, His, Cys) #status predicted
 F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0% Score 9; DB 1; Length 391;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 GGMNRRPIL 283
 Db 242 GGMNRRPIL 250
 |||||

RESULT 11

JC6193
 tumor suppressor p53 - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
 C:Accession: JC6193
 R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.
 Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.
 A:Reference number: JC6193; MUID:97208869; PMID:9055811
 A:Accession: JC6193
 A:Molecule type: mRNA
 A:Residues: 1-391 <LEA>
 A:Cross-references: EMBL:X90592; NID:91532043; PIDN:CAA62216.1; PID:91532044
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: tumor

Query Match 2.0% Score 9; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 GGMNRRPIL 283
 Db 241 GGMNRRPIL 249
 |||||

RESULT 12

DNHU53
 cellular tumor antigen p53 [validated] - human
 N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor
 C:Species: Homo sapiens (man)
 C>Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
 C:Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397.
 4905; I58354; I78850; I52681; S60153
 R:Lamb, P.; Crawford, L.
 Mol. Cell. Biol. 6, 1379-1385, 1986
 A:Title: Characterization of the human p53 gene.
 A:Reference number: A25224; MUID:87064416; PMID:2946935
 A:Accession: A25224
 A:Molecule type: DNA
 A:Residues: 1-393 <LAM>
 A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:9189460; PIDN:AAA59987.1;
 R:Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
 Gene 70, 245-252, 1988
 A:Title: A variation in the structure of the protein-coding region of the human p53 gene
 A:Reference number: JT0436; MUID:89108008; PMID:2905688
 A:Accession: A43073
 A:Molecule type: DNA
 A:Residues: 1-393 <BUCL>
 A:Cross-references: EMBL:M22898; NID:9189474
 A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro
 A:Accession: JT0436
 A:Molecule type: DNA
 A:Residues: 1-71, 'P', 73-393 <BUC2>
 A:Cross-references: EMBL:M22898; NID:9189474; PIDN:AAA59988.1; PID:9189476
 R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S40773
 A:Accession: S40773
 A:Molecule type: DNA
 A:Residues: 1-393 <CHU>
 A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
 R:Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
 EMBO J. 3, 3257-3262, 1984
 A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the
 A:Reference number: S42669; MUID:85126934; PMID:6396087
 A:Accession: S42669
 A:Molecule type: mRNA
 A:Residues: 101-393 <MKII>
 A:Cross-references: EMBL:X01405; NID:935215; PIDN:CAA25652.1; PID:9642241
 R:Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
 EMBO J. 4, 1251-1255, 1985
 A:Title: Human p53 cellular
 A:Reference number: A22837; MUID:85230577; PMID:4006916
 A:Accession: A22837
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-393 <ZAK>
 A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210

R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tu
A:Reference number: A55060; MUID:85267676; PMID:3894933
A:Accession: A55060
A:Molecule type: mRNA
A:Residues: 1-71,'P',73-272,'H',274-393 <HAR>
A:Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A:Experimental source: clone pR4-2, cell line A431
R:Harris, N.; Brill, E.; Shohat, O.; Frokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664
A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78,'T',80-393 <HAR1>
A:Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71,'P',73-78,'T',80-393 <HAR2>
A:Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Maciashewski, G.J.; Tuck, S.; Plm, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71,'P',73-79 <MKI2>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MKI3>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: 138082; MUID:92007731; PMID:1915267
A:Accession: 138082
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189,'L',189-393 <F02>
A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: 138083
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192,'R',194-393 <F02>
A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
A:Accession: 138084
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <F03>
A:Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437
A:Accession: 138085
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245,'T',247-393 <F04>
A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439
A:Accession: 138086
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236,'I',238-393 <F05>
A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
A:Accession: 138087
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247,'Q',249-393 <F06>
A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
A:Accession: 138088
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-71,'P',73-237,'Y',239-393 <F07>
A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
A:Accession: 138089
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247,'Q',249-393 <F08>
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A:Accession: 138090
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71,'P',73-162,'H',164-393 <F09>
A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449
A:Accession: 138091
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212,'Q',214-393 <F10>
A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A:Accession: 138092
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-253,'D',255-393 <F11>
A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A:Note: all sequences submitted to the EMBL/Genbank/DBJ databases June 1991
R:Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Alu polymorphism intragenic to the tp53 gene.
A:Reference number: 138093; MUID:92107726; PMID:1762941
A:Accession: 138093
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakata
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell
A:Reference number: A44905; MUID:92034678; PMID:1933850
A:Accession: A44905
A:Molecule type: DNA
A:Residues: 246-247,'W',249-250 <YAM>
A:Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830
A:Note: sequence extracted from NCI backbone (NCBI:63157, NCBIP:63158)
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A:Title: Use of the single strand conformation polymorphism technique and PCR to dete
A:Reference number: 158354; MUID:91296386; PMID:1648702
A:Accession: 158354
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 244-247,'W',249-252 <HEN1>
A:Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1; PID:g232814
A:Accession: 178850
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 274-277,'S',279-282 <HEN2>
A:Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lympho
A:Reference number: 152681; MUID:94036762; PMID:8221626
A:Accession: 152681
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 327-331,'D',327-331 <CHO>
A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-1
R:Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenberg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fra
A:Reference number: S60151; MUID:96133682; PMID:8552047
A:Accession: S60153
A:Molecule type: DNA

A:Residues: 3-44 <PET>
R: Dang, C.V.; Lee, W.M.F.

J. Biol. Chem. 264, 18019-18023, 1989

A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 2.0%; Score 9; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283

Db 244 GGMNRRPIL 252

RESULT 13

S06594

cellular tumor antigen p53 - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S06594

R:Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989

A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.

A:Reference number: S06594; MUID:90045967; PMID:2530498

A:Accession: S06594

A:Molecule type: mRNA

A:Residues: 1-393 <RIG>

A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph

F:176,179,236,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0%; Score 9; DB 1; Length 393;

Best Local Similarity 100.0%; Pred. No. 0.82;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283

Db 244 GGMNRRPIL 252

RESULT 14

A56346

transcription factor kni - fruit fly (Drosophila virilis)

C:Species: Drosophila virilis

C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Dec-1999

C:Accession: A56346

R:Gerwin, N.; La Rosee, A.; Sauer, F.; Halbritter, H.P.; Neumann, M.; Jaekle, H.; Naube

Mol. Cell. Biol. 14, 7899-7908, 1994

A:Title: Functional and conserved domains of the Drosophila transcription factor encoded

A:Reference number: A56346; MUID:95059019; PMID:7969130

A:Accession: A56346

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-481 <GER>

A:Cross-references: GB:L36177; NID:g537507; PID:g537508

A>Note: authors translated the codon GCG for residue 403 as Pro

C:Genetics:

A:Gene: knirps

A:Cross-references: FlyBase:FBgn0013118

A:Introns: 26/3

Query Match

Best Local Similarity 100.0%; Score 9; DB 2; Length 481;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 QQQQQQHQL 406

Db 135 QQQQQQHQL 143

RESULT 15

A30168

homeotic protein Labial - fruit fly (Drosophila sp.)

C:Species: Drosophila sp.

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000

C:Accession: A30168; A24149

R:Diederich, R.J.; Merrill, V.K.L.; Pultz, M.A.; Kaufman, T.C.

Genes Dev. 3, 399-414, 1989

A:Title: Isolation, structure, and expression of Labial, a homeotic gene of the anten

A:Reference number: A30168; MUID:89252817; PMID:2566560

A:Accession: A30168

A:Molecule type: mRNA; DNA

A:Residues: 1-629 <DIE>

R:Hoey, T.; Doyle, H.J.; Harding, K.; Wedeen, C.; Levine, M.

Proc. Natl. Acad. Sci. U.S.A. 83, 4809-4813, 1986

A:Title: Homeo box gene expression in anterior and posterior regions of the Drosophil

A:Reference number: A24149; MUID:86259687; PMID:3014511

A:Accession: A24149

A:Molecule type: DNA

A:Residues: 501-561 <HOE>

C:Genetics:

A:Gene: FlyBase:lab

A:Cross-references: FlyBase:FBgn0002522

A:Introns: 406/1; 544/3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:502-558/Domain: homeobox homology <HOX>

Query Match

Best Local Similarity 100.0%; Score 9; DB 2; Length 629;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 QQQQQQHQL 407

Db 51 QQQQQQHQL 59

Search completed: June 24, 2003, 22:29:48

Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:24:26 ; Search time 16 seconds
(without alignments)
823.842 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 448

Sequence: 1 MSQSTQTNELSPVFOH.....PKQSDVFRHKKPNRSVYP 448

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCRU5_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	448	US-09-643-597-340	Sequence 340, App
2	410	91.5	516	US-09-643-597-344	Sequence 344, App
3	410	91.5	641	US-09-643-597-339	Sequence 339, App
4	410	91.5	680	US-09-643-597-342	Sequence 342, App
5	341	76.1	461	US-09-643-597-343	Sequence 343, App
6	272	60.7	586	US-09-643-597-338	Sequence 338, App
7	269	60.0	356	US-09-643-597-341	Sequence 341, App
8	191	42.6	586	US-09-643-597-152	Sequence 152, App
9	22	4.9	635	US-09-081-975-3	Sequence 3, Appli
10	9	2.0	71	US-09-146-054-9	Sequence 9, Appli
11	9	2.0	71	US-09-664-977A-9	Sequence 9, Appli
12	9	2.0	169	US-08-094-071-3	Sequence 3, Appli
13	9	2.0	169	PCT-US92-00878-3	Sequence 3, Appli
14	9	2.0	170	US-08-094-071-2	Sequence 2, Appli
15	9	2.0	170	US-08-094-071-5	Sequence 5, Appli
16	9	2.0	170	US-08-094-071-6	Sequence 6, Appli
17	9	2.0	170	US-08-094-071-7	Sequence 7, Appli
18	9	2.0	170	PCT-US92-00878-2	Sequence 2, Appli
19	9	2.0	170	PCT-US92-00878-5	Sequence 5, Appli
20	9	2.0	170	PCT-US92-00878-6	Sequence 6, Appli
21	9	2.0	170	PCT-US92-00878-7	Sequence 7, Appli
22	9	2.0	271	US-09-414-436-1	Sequence 1, Appli
23	9	2.0	319	US-08-983-035A-42	Sequence 42, Appl
24	9	2.0	335	US-08-983-035A-44	Sequence 44, Appl
25	9	2.0	353	US-08-983-035A-40	Sequence 40, Appl
26	9	2.0	363	US-08-697-221-17	Sequence 17, Appl
27	9	2.0	363	US-08-697-221-18	Sequence 18, Appl

28	9	2.0	363	2	US-08-697-221-21	Sequence 21, Appl
29	9	2.0	363	2	US-08-697-221-22	Sequence 22, Appl
30	9	2.0	363	2	US-08-697-221-23	Sequence 23, Appl
31	9	2.0	363	2	US-08-697-221-24	Sequence 24, Appl
32	9	2.0	363	4	US-08-983-035A-26	Sequence 26, Appl
33	9	2.0	374	4	US-08-983-035A-28	Sequence 28, Appl
34	9	2.0	381	4	US-09-257-580-2	Sequence 2, Appli
35	9	2.0	381	4	US-08-983-035A-36	Sequence 36, Appl
36	9	2.0	390	1	US-08-347-792-15	Sequence 15, Appl
37	9	2.0	390	1	US-08-431-357-15	Sequence 15, Appl
38	9	2.0	390	4	US-08-392-542-3	Sequence 3, Appli
39	9	2.0	390	4	US-08-894-327-3	Sequence 3, Appli
40	9	2.0	390	4	US-09-685-027-3	Sequence 3, Appli
41	9	2.0	390	5	PCT-US95-15353-15	Sequence 15, Appl
42	9	2.0	393	1	US-08-047-041A-25	Sequence 25, Appl
43	9	2.0	393	1	US-08-047-041A-26	Sequence 26, Appl
44	9	2.0	393	1	US-08-047-041A-27	Sequence 27, Appl
45	9	2.0	393	1	US-08-047-041A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-643-597-340
; Sequence 340, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455041
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2006-08-21
; NUMBER OF SEQ ID NOS: 369
; SUMMARY: FASTSEQ for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-340

Query Match	100.0%;	Score 448;	DB 4;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSQSTQTNELSPVFOHINDFLEQPCISVQPIDINFDVDEPSEDATNKIETSMDCIRMQ	60	
Db	1	MSQSTQTNELSPVFOHINDFLEQPCISVQPIDINFDVDEPSEDATNKIETSMDCIRMQ	60	
Qy	61	DSLDSDPMWQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120	
Db	61	DSLDSDPMWQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120	
Qy	121	SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180	
Db	121	SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180	
Qy	181	PGQAVIRAMPYKKAHEHTEVVVKPCPNHLSREFNEGOIAPPSHLIRVEGSHQAQYVEDP	240	
Db	181	PGQAVIRAMPYKKAHEHTEVVVKPCPNHLSREFNEGOIAPPSHLIRVEGSHQAQYVEDP	240	
Qy	241	ITGRQSVLPVPEPPQVGTEFTTVLYNFCNCSVCGMNRRPILIIIVTLETRDGOVLGRRC	300	

7/2 seb
Not claimed
priority date 8/12/2002

us-09-670-568b-1.oli.ra

Mon Jun 30 08:33:12 2003

361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQK 410
 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQK 410

241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 300
 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360
 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360
 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQKLLSACFRNE 420
 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQKLLSACFRNE 420
 421 LVEPRRETQKSDVFFRHSKPPNRSVYP 448
 421 LVEPRRETQKSDVFFRHSKPPNRSVYP 448

RESULT 2
 US-09-643-597-344 Application US/09643597

; Sequence 344, Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 344

; LENGTH: 516

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-643-597-344

Query Match 91.5%; Score 410; DB 4; Length 516;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative

QY 1 MSQSTQTNFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSQSTQTNFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 180
 DB 121 SPSPAIPSNITDYPGPHSFDFVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 121 SPSPAIPSNITDYPGPHSFDFVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 240
 DB 181 PGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 181 PGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 300
 QY 241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 300
 DB 241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 360
 QY 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360
 DB 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360

RESULT 4

US-09-643-597-342

; Sequence 342, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

Query Match 91.5%; Score 410; DB 4; Length 641;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative

QY 1 MSQSTQTNFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSQSTQTNFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 61 DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 180
 DB 121 SPSPAIPSNITDYPGPHSFDFVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 121 SPSPAIPSNITDYPGPHSFDFVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 240
 DB 181 PGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 181 PGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 300
 QY 241 ITGRQSVLPVPEPQVGTFTVLYNFMNCSSCVGMNRRPILIVTLETRDQVLRRC 300
 DB 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360
 QY 301 FEARICACGRDRKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGHIQMTSIIKKRSPDDE 360
 DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQK 410
 DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHHLLQK 410

;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSeq for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/081,975
;; FILING DATE: 12-MAY-1998
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/046,207
;; FILING DATE: 12-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eisenstein, Ronald I
;; REGISTRATION NUMBER: 30,628
;; REFERENCE/DOCKET NUMBER: 47400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-345-6054
;; TELEFAX: 617-345-1300
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 635 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-081-975-3

Query Match 4.9%; Score 22; DB 4; Length 635;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 LYNFMCNSSCVGGMNRRLPIII 285

Db 253 LYNFMCNSSCVGGMNRRLPIII 274

RESULT 10

US-09-146-054-9

; Sequence 9, Application US/09146054

; Patent No. 632970

; GENERAL INFORMATION:

; APPLICANT: Little, Daniel

; APPLICANT: Higgins, G. Scott

; APPLICANT: Koster, Hubert

; APPLICANT: Lough, David

; APPLICANT: SEQUENOM, INC.

; TITLE OF INVENTION: Mass Spectrometric Detection of Polypeptides

; FILE REFERENCE: 2016B

; CURRENT APPLICATION NUMBER: US/09/146,054

; CURRENT FILING DATE: 1998-09-02

; EARLIER APPLICATION NUMBER: 08/922,201

; EARLIER FILING DATE: 1997-09-02

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 71

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: REPEAT

; LOCATION: (14)..(38)

; OTHER INFORMATION: "gln" repeat region associated with spinal

; FEATURE: cerebellar ataxia 1 (SCA-1)

; NAME/KEY: REPEAT

; LOCATION: (66)..(71)

; OTHER INFORMATION: His-6 "tag"

US-09-146-054-9

Query Match 2.0%; Score 9; DB 4; Length 71;

Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 398 QQQQQQH 406

Db 20 QQQQQQH 28

RESULT 11

US-09-664-977A-9

; Sequence 9, Application US/09664977A

; Patent No. 6387628

; GENERAL INFORMATION:

; APPLICANT: Little, Daniel

; APPLICANT: Higgins, G. Scott

; APPLICANT: Koster, Hubert

; APPLICANT: Lough, David

; TITLE OF INVENTION: Mass Spectrometric Detection of Polypeptides

; FILE REFERENCE: 2016C

; CURRENT APPLICATION NUMBER: US/09/664,977A

; CURRENT FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: 09/146,054

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 08/922,201

; PRIOR FILING DATE: 1997-09-02

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 71

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: REPEAT

; LOCATION: (14)..(38)

; OTHER INFORMATION: "gln" repeat region associated with spinal

; FEATURE: cerebellar ataxia 1 (SCA-1)

; NAME/KEY: REPEAT

; LOCATION: (66)..(71)

; OTHER INFORMATION: His-6 "tag"

US-09-664-977A-9

Query Match 2.0%; Score 9; DB 4; Length 71;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 398 QQQQQQH 406

Db 20 QQQQQQH 28

RESULT 12

US-08-094-071-3

; Sequence 3, Application US/08094071

; Patent No. 6083709

; GENERAL INFORMATION:

; APPLICANT: Reynolds, Frederick H.

; APPLICANT: Sorvillo, John M.

; APPLICANT: Zehed, Ron J.

; APPLICANT: Stephenson, John R.

; TITLE OF INVENTION: Immuncassay for Detection of

; TITLE OF INVENTION: mutant p53 polypeptide in

; TITLE OF INVENTION: biological fluids

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

us-09-670-568b-1.oli.ra1

Mon Jun 30 08:33:12 2003

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,071
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86.111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Bartek, J.
AUTHORS: Iggo, R.
AUTHORS: Lane, D. P.
TITLE: Genetic and immunochemical analysis of mutant p53 in
TITLE: human breast cancer cell lines
JOURNAL: Oncogene
VOLUME: 5
PAGES: 893-899
DATE: 1990
US-08-094-071-3
Query Match 2.0%; Score 9; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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QY 275 GGMNRRPIL 283
Db 127 GGMNRRPIL 135
RESULT 13
PCT-US92-00878-3
Sequence 3, Application PC/TUS9200878
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Sorvillo, John M.
APPLICANT: Zeheb, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of mutant p53
TITLE OF INVENTION: polypeptide in biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper and Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00878
FILING DATE: 19920131
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86.111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525

```

TELEX: 422523 coop ui
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Bartek, J.
AUTHORS: Iggo, R. P.
AUTHORS: Lane, D. P.
TITLE: Genetic and immunochemical analysis of mutant p53 in
TITLE: human breast cancer cell lines
JOURNAL: Oncogene
VOLUME: 5
PAGES: 893-899
DATE: 1990
PCT-US92-00878-3

Query Match 2.0%; Score 9; DB 5; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GGMNRRPIL 283
Db 127 GGMNRRPIL 135

RESULT 14

US-08-094-071-2
Sequence 2, Application US/08094071
Patent No. 6083709
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Sorvilio, John M.
APPLICANT: Zehnb, Ron J.
TITLE OF INVENTION: Immunoassay for Detection of
TITLE OF INVENTION: mutant p53 polypeptide in
TITLE OF INVENTION: biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,071
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837

FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86.111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Bartek, J.
AUTHORS: Iggo, R.
AUTHORS: Lane, D. P.
TITLE: Genetic and immunochemical analysis of
TITLE: mutant p53 in human breast cancer cell lines
JOURNAL: Oncogene
VOLUME: 5
PAGES: 893-899
DATE: 1990
US-08-094-071-2

Query Match 2.0%; Score 9; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GGMNRRPIL 283
Db 128 GGMNRRPIL 136

RESULT 15

US-08-094-071-5
Sequence 5, Application US/08094071
Patent No. 6083709
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Sorvilio, John M.
APPLICANT: Zehnb, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of
TITLE OF INVENTION: mutant p53 polypeptide in

;; TITLE OF INVENTION: biological fluids
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper and Dunham
;; STREET: 30 Rockefeller Plaza
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10112
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/094,071
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 719,172
;; FILING DATE: 21-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 649,566
;; FILING DATE: 01-FEB-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 298,776
;; FILING DATE: 17-JAN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 298,837
;; FILING DATE: 18-JAN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 885,627
;; FILING DATE: 23-JUL-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 767,862
;; FILING DATE: 21-AUG-1985
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU 61540/86
;; FILING DATE: 18-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: CA 516,260
;; FILING DATE: 19-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 86.111 527.7
;; FILING DATE: 20-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 195121/86
;; FILING DATE: 20-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: NZ 217,209
;; FILING DATE: 14-AUG-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 23384-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 977-9550
;; TELEFAX: (212) 664-0525
;; TELEX: 422523 COOP U1
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 170 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; IMMEDIATE SOURCE:
;; CLONE: activated p53 oncogene
;; PUBLICATION INFORMATION:
;; AUTHORS: Bartek, J.
;; AUTHORS: 1990, R.

;; AUTHORS: Lane, D. P.
;; TITLE: Genetic and immunochemical analysis of mutant p53 in
;; human breast cancer cell lines
;; JOURNAL: Oncogene
;; VOLUME: 5
;; PAGES: 893-899
;; DATE: 1990
;; US-08-094-071-5

Query Match 2.0%; Score 9; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 275 GGMNRRPIL 283
| | | | |
Db 128 GGMNRRPIL 136

Search completed: June 24, 2003, 22:29:23
Job time : 17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:35:33 ; Search time 7008 Seconds
(without alignments)
11694.278 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

Sequence: 1 tctgtgatcaagaagcgt.....gcattgtgtttaaaagaaa 2816

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

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2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

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31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2816	100.0	2816	6	AX365940	AX365940 Sequence
2	2816	100.0	2816	6	BD000748	BD000748 Chimera g
3	2816	100.0	2816	9	AB016072	AB016072 Homo sapi
4	1440	51.1	1516	9	FL16756S15	FL16756S15 Homo sapi
5	1433	50.9	180055	9	AC063939	AC063939 Homo sapi
6	1376	48.9	2031	9	AF116771	AF116771 Homo sapi
7	1376	48.9	2270	6	AX365939	AX365939 Sequence
8	1376	48.9	2270	6	BD000749	BD000749 Chimera g
9	1376	48.9	2270	9	AB016073	AB016073 Homo sapi
10	1347	47.8	1347	9	AF075428	AF075428 Homo sapi
11	1275	45.3	4846	6	AX009538	AX009538 Sequence
12	1275	45.3	4849	6	AX365942	AX365942 Sequence
13	1275	45.3	4849	9	HSA16961	Y16961 Homo sapien
14	1232	43.8	1551	6	AX365944	AX365944 Sequence
15	1232	43.8	1551	9	AF075432	AF075432 Homo sapi
16	1232	43.8	1926	9	AF075430	AF075430 Homo sapi
17	1141	40.5	1182	9	AF075429	AF075429 Homo sapi
18	1026	36.4	1386	6	AX365943	AX365943 Sequence
19	1026	36.4	1386	9	AF075433	AF075433 Homo sapi
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22	975	34.6	2082	6	AX365941	AX365941 Sequence
23	975	34.6	2082	9	AF061512	AF061512 Homo sapi
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25	822	29.2	2820	6	AX365938	AX365938 Sequence
26	822	29.2	2820	9	AB010153	AB010153 Homo sapi
27	720	25.6	1506	9	AB042841	AB042841 Homo sapi
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29	370	13.1	970	9	HSP63G13	AF124540 Homo sapi
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31	256	9.1	1193	9	HSP63G04	AF124531 Homo sapi
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42	119	4.2	865	9	HSP63G06	AF124533 Homo sapi
43	113	4.0	627	9	FL16756S07	AF116762 Homo sapi
44	101	3.6	428	9	FL16756S01	AF116756 Homo sapi
45	90	3.2	835	9	HSP63G01	AF124528 Homo sapi

ALIGNMENTS

RESULT 1
AX365940

LOCUS

DEFINITION

AX365940

ACCESSION

AX365940.1

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

AX365940 Sequence 333 from Patent WO0200174.
2816 bp DNA linear PAT 15-FEB-2002

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Wang, T., Wang, A., Skelky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,
McNeill, P.D., Fanger, M., Retter, M.W., Marnierakis, N., Fanger, G.R.,
Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.

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RESULT 2

BD000748 BD000748 2816 bp DNA linear PAT 31-JAN-2002
LOCUS Chimera gene and chimera protein of p53 family.
DEFINITION

BD000748

ACCESSION

BD000748.1 GI:18623861

VERSION

JP 2000354488-A/1.

KEYWORDS

Homo sapiens

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2816)

Ikawa.Y., Ikawa.S. and Tatewaki.M.

Chimera gene and chimera protein of p53 family

Patent: JP 2000354488-A 1 26-DEC-2000;

COMMENT
OS Homo sapiens (human)
PN JP 2000354488-A/1
PD 26-DEC-2000
PF 09-APR-1999 JP 1999139034

PR YOJI IKAWA, SHUNTARO IKAWA, MASUO TATEWAKI
PC C12N15/09, C07K14/82, C07K19/00, C12N15/00
CC

Key Location/Qualifiers
CDS (145)..(1488)
FT polyA_signal (2786)..(2791).

FEATURES
source
1..2816
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 781 a 658 c 619 g 758 t
ORIGIN

Query Match 100.0%; Score 2816; DB 6; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTTGATATCAAAAGACAGATTGAAGAAATGAATTTTGAACATTTACCGGTGTGCCACCT 60
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Db 1 TCGTTGATATCAAAAGACAGATTGAAGAAATGAATTTTGAACATTTACCGGTGTGCCACCT 60
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QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTGTAGAAAACCCAGCTCATTTCTCTGG 120
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Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTGTAGAAAACCCAGCTCATTTCTCTGG 120
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Db 361 ACGAACCTGGGGCTCTGAAACAGCATGGACAGAGATTTCAGAACGGCTCTCTGTCACC 420
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Db 961 TGTGTTGGAGGATGAACCGCCCTCCAAATTTTAATCATTTGTTACTCTGGAACACAGAGAT 1020
QY 1021 GGCAAGTCTTGGGCGAGCTGCTTTGAGGCCCGGATCTGTGCTTTGCCAGGAAGAGAC 1080
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QY 1141 GATGGTACGAAGCGCCGTTTCTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGGTACGAAGCGCCGTTTCTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATCTTACCAGTAGAGGGCGGTGAGACTTAT 1260
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Db 1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAATCATGACAGTACCTTCTCAGCACACA 1320
QY 1321 ATTGAACGTACAGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
Db 1321 ATTGAACGTACAGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
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Db 1381 CTTTCAGCTGCTTCAGGATGAGCTTTGGAGCCCGGAGAGAACTCCAAACAACTCT 1440
QY 1441 GAGCTCTCTTTAGACATTCGAAGCCCAAGCCGATCAGTGTACCCATAGAGCCCTATC 1500
Db 1441 GAGCTCTCTTTAGACATTCGAAGCCCAAGCCGATCAGTGTACCCATAGAGCCCTATC 1500
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RESULT 3

AB016072

LOCUS

DEFINITION

AB016072

ACCESSION

AB016072.1

VERSION

KEYWORDS

AB016072 2816 bp mRNA linear PRI 06-FEB-1999
Homo sapiens mRNA for p51A, complete cds.
AB016072
AB016072.1 GI:3510327
p51A.

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QY 1921 AAAAAAGTTGTTATTTGCTCTGTCATGAAGTAAAGTTGTAGTGAAGTGTGAGAGCTCAGTCAGA 1980
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RESULT 4
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DEFINITION Homo sapiens p51 gene, exon 15 and complete cds, alternatively
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ACCESSION AF116770
VERSION AF116770.1 GI:7248444
KEYWORDS 15 of 15
SEGMENT Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1516)
AUTHORS Tan, M., Shimizu, K., Kawahara, C., Kohno, T., Ishimoto, O., Ikawa, S.
and Yokota, J.
TITLE Mutation and expression of the p51 gene in human lung cancer
JOURNAL Neoplasia 1 (1), 71-79 (1999)
MEDLINE 20388515
PUBMED 10935472
REFERENCE 2 (bases 1 to 1516)
AUTHORS Tan, M., Shimizu, K., Kohno, T., Ikawa, S. and Yokota, J.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1998) Biology Division, National Cancer Center
Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045,
Japan
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ACCESSION AC063939
VERSION AC063939.15 GI:18958587
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1 (bases 1 to 180055)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
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Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
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Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
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Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.K., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Neilson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonalke, F., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 180055)
 Worley, K.C.

Direct Submission
 Submitted (22-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 180055)
 Worley, K.C.

Direct Submission
 Submitted (27-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 180055)
 Worley, K.C.

Direct Submission
 Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Feb 27, 2002 this sequence version replaced qi:17933791.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2031)
Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.
Mutations and expression of the p51 gene in human lung cancer
Unpublished
2 (bases 1 to 2031)
Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.
Direct Submission
Submitted (28-DEC-1998) Biology Division, National Cancer Center
Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045,
Japan

FEATURES

source

Location/Qualifiers
1..2031
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CDS

BASE COUNT 543 a 591 c 454 g 443 t

ORIGIN

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RESULT 7

AX365939

LOCUS

DEFINITION

AX365939

VERSION

AX365939.1

SOURCE

human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A.,

AX365939 Sequence 332 from Patent WO0200174.

GI:18697448

2270 bp DNA 1linear PAT 15-FEB-2002

human

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A.,

Mcneill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R.,
Vedick, T.S., Carter, D., Watanabe, Y., and Peckham, D.W.
Compositions and methods for the therapy and diagnosis of lung
cancer
Patent: WO 0200174-A 332 03-JAN-2002;
CORIXA CORPORATION (US)
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Query Match 48.9%; Score 1376; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Chimera gene and chimera protein of p53 family.
DEFINITION BD000749
ACCESSION BD000749
VERSION BD000749.1 GI:18623862
KEYWORDS JP 2000354488-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2270)
AUTHORS Ikawa, Y., Ikawa, S. and Tatewaki, M.
TITLE Chimera gene and chimera protein of p53 family
JOURNAL Patent: JP 2000354488-A 2 26-DEC-2000;
YOJI IGAWA, OTSUKA PHARMACEUTICAL CO LTD
OS Homo sapiens (human)
PN JP 2000354488-A/2
PD 26-DEC-2000
PF 09-APR-1999 JP 1999139034
PR
PI YOJI IGAWA, SHUNTARO IKAWA, MASUO TATEWAKI
CC C12N15/09, C07K14/82, C07K19/00, C12N15/00
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BASE COUNT 595 a 677 c 500 g 498 t
ORIGIN
Query Match 48.9%; Score 1376; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION	AB016073		
VERSION	AB016073.1	GI:3510329	
KEYWORDS	p51b.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (sites) Osada,M., Ohba,M., Kawahara,C., Ishioka,C., Kanamaru,R., Katoh,I., Ikawa,Y., Nimura,Y., Nakagawara,A., Obinata,M. and Ikawa,S.		
TITLE	Cloning and functional analysis of human p51, which structurally and functionally resembles p53		
JOURNAL	Nat. Med. 4 (7), 829-843 (1998)		
MEDLINE	98324755		
REFERENCE	2 (bases 1 to 2270) Ikawa,S. and Osada,M.		
AUTHORS	Direct Submission		
TITLE	Submitted (10-JUL-1998) Shuntaro Ikawa, Institute of Development, Aging and Cancer, Department of Cell Biology; 4-1 Seiry-machi, Sendai, Miyagi 980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp, Tel:81-22-717-8484, Fax:81-22-717-8488)		
JOURNAL	Location/Qualifiers		
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BASE COUNT	595 a 676 c 501 g 498 t		
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Query Match 48.9%; Score 1376; DB 9; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Homo sapiens TA p63 gamma mRNA, complete cds.
DEFINITION AF075428
ACCESSION AF075428
VERSION AF075428.1 GI:3695077
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1347)
AUTHORS Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V.,
Andrews,N.C., Caput,D. and McKeon,F.
TITLE p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
JOURNAL
MEDLINE 98448095
PUBMED 9774969
REFERENCE 2 (bases 1 to 1347)
AUTHORS Yang,A., Kaghad,M., Caput,D. and McKeon,F.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
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Qy	985	CCAATTTTAAATCAATTTACTCTGGAACCCAGAGATGGCAAGTCTCTGGGCCAGCGTGC	1044						
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Qy	1045	TTTGAAGCCCGGATCTGTGTTGCCAGGAAGACAGAGGCGGATGAAGATAGCATC	1104						
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Db	1081	CTGTTTATCTTACCAGTGGGGCCGCTGAGACTTATGAATGCTGTTGAAGATCAAGAG	1140						
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RESULT 11									
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LOCUS	AX009538	4846 bp	DNA	linear	PAT 06-SEP-2000				
DEFINITION	Sequence 2 from Patent WO9961610.								
ACCESSION	AX009538								
VERSION	AX009538.1	GI:9956812							
KEYWORDS	synthetic construct.								
SOURCE	synthetic construct.								
ORGANISM	artificial sequences.								
REFERENCE	1 (bases 1 to 4846)								
AUTHORS	Bamberg, C., Paul, D., Augustin, M. and Schmale, H.								
TITLE	Tumour suppressor genes of the p53 family								
JOURNAL	Patent: WO 9961610-A 2 02-DEC-1999;								
	BAMBERGER CASIMIR (DE); PAUL DIETER (DE); AUGUSTIN MARTIN (DE);								
	SCHMALE HARTWIG (DE); FRAUNHOFER GES FORSCHUNG (DE)								
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RESULT 12
AX365942
LOCUS AX365942 4849 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 335 from Patent WO0200174.
ACCESSION AX365942
VERSION AX365942.1 GI:18697451

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wang, T., Wang, A., Skeiky, Y. A., Li, S. X., Kalos, M. D., Henderson, R. A.,
Mcneill, P. D., Fanger, N., Retter, M. W., Marnerakis, M., Fanger, G. R.,
Vedvick, T. S., Carter, D., Watanabe, Y. and Peckham, D. W.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0200174-A 335 03-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1. 4849
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/db_xref="taxon:9606"
BASE COUNT 1377 a 1076 c 988 g 1407 t 1 others
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Query Match 45.3%; Score 1275; DB 6; Length 4849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS HSA16961
DEFINITION Homo sapiens mRNA for KET protein.
ACCESSION Y16961
VERSION Y16961.1
KEYWORDS KET gene; KET protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4849)
Direct Submission
Submitted (24-MAR-1998) H. Schmale, Institut f. Zellbiochemie und,
Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf,
Martinstrasse 52, D-20246 Hamburg, FRG
2 (bases 1 to 4849)
Augustin, M., Bamberger, C., Paul, D. and Schmale, H.
Cloning and chromosomal mapping of the human p53-related KET gene
to chromosome 3q27 and its murine homolog Ket to mouse chromosome
16
Mamm. Genome 9 (11), 899-902 (1998)
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 15
AF075432 1551 bp mRNA linear PRI 04-OCT-1998
LOCUS Homo sapiens TA p63 beta mRNA, complete cds.
DEFINITION AF075432
ACCESSION AF075432.1 GI:3695085
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1551)
Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V.,
Andrews,N.C., Caput,D. and McKeon,F.
p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
98448095
9774969
REFERENCE 2 (bases 1 to 1551)
AUTHORS Yang,A., Kaghad,M., Caput,D. and McKeon,F.
TITLES Direct Submission
JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
FEATURES
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QY 205 GATTTCCTGGAACAGCCTATATCTTCAGTTCAGCCCATTTGACATTGACATTTGTTGGATGAA 264
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61 GATTTCCTGGAACAGCCTATATCTTCAGTTCAGCCCATTTGACATTGACATTTGTTGGATGAA 120
```

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QY 265 CCATCAGAGAGTGTGCGACAAACAGATTGAGATTAGCATGAGCTGTATCCGATGCAG 324
Db
121 CCATCAGAGAGTGTGCGACAAACAGATTGAGATTAGCATGAGCTGTATCCGATGCAG 180
QY 325 GACTCGGACCTAGTGTACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGTGAACAGC 384
Db
181 GACTCGGACCTAGTGTACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGTGAACAGC 240
QY 385 ATGGACACGAGATTACAGAACGGCTCTCTGTCCACAGTCCCTATATAACACACACACAGCGG 444
Db
241 ATGGACACGAGATTACAGAACGGCTCTCTGTCCACAGTCCCTATATAACACACACACAGCGG 300
QY 445 CAGAACAGCGGTACGCGGCGCTTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 504
Db
301 CAGAACAGCGGTACGCGGCGCTTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 360
QY 505 TCTCCATCACCGCGCATCCCTCCACACACCGGACTACCCAGGCGCCGACAGTTTCGACGTC 564
Db
361 TCTCCATCACCGCGCATCCCTCCACACACCGGACTACCCAGGCGCCGACAGTTTCGACGTC 420
QY 565 TCCTTCCAGCAGTTCGAGCACCGCCCAAGTCGGCCACCTGGACGCTATTCCCACTGAACCTGAAG 624
Db
421 TCCTTCCAGCAGTTCGAGCACCGCCCAAGTCGGCCACCTGGACGCTATTCCCACTGAACCTGAAG 480
QY 625 AAACCTCTACTGTCCTCAAAATGTCAAAGACATGCCCTCCAGATCAAGGTGATGATGATGATG 684
Db
481 AAACCTCTACTGTCCTCAAAATGTCAAAGACATGCCCTCCAGATCAAGGTGATGATGATGATG 540
QY 685 CCTCAGGAGCTGTTATTCGCGCGCATGCTGTCTACAAAAAGCTGAGCACGTCACGAGAG 744
Db
541 CCTCAGGAGCTGTTATTCGCGCGCATGCTGTCTACAAAAAGCTGAGCACGTCACGAGAG 600
QY 745 GTGGTGAACGGTGCCTCCCAACCATGAGCTGAGCGCTGAATTCACACAGGAGCAGATTGCC 804
Db
601 GTGGTGAACGGTGCCTCCCAACCATGAGCTGAGCGCTGAATTCACACAGGAGCAGATTGCC 660
QY 805 CCTCCTAGTTCATTTGATTGAGTGTAGAGGGGAAACAGCCATGCCAGTATGTAGAGATGCC 864
Db
661 CCTCCTAGTTCATTTGATTGAGTGTAGAGGGGAAACAGCCATGCCAGTATGTAGAGATGCC 720
QY 865 ATCAGAGGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGCTTGGCACTGATATTC 924
Db
721 ATCAGAGGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGCTTGGCACTGATATTC 780
QY 925 AGCAGAGTCTTGTACAAATTTGATGTAAACAGCAGTGTGTGGAGGGGATGAACCCCGT 984
Db
781 AGCAGAGTCTTGTACAAATTTGATGTAAACAGCAGTGTGTGGAGGGGATGAACCCCGT 840
QY 985 CCAATTTTAACTGTTTACTCTGGAACACAGAGATGGCAAGTCTGGGCGCAGCCTGC 1044
Db
841 CCAATTTTAACTGTTTACTCTGGAACACAGAGATGGCAAGTCTGGGCGCAGCCTGC 900
QY 1045 TTTGAGGCGCGGATCTGCTGTCGCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
Db
901 TTTGAGGCGCGGATCTGCTGTCGCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 960
QY 1105 AGAAACACACAGTTTTCGGACAGTACAAAGACGGTGTGATGTCAGGAAGCGCCGCTTTCGT 1164
Db
961 AGAAACACAGTTTTCGGACAGTACAAAGACGGTGTGATGTCAGGAAGCGCCGCTTTCGT 1020
QY 1165 CAGAACACACATGGTATTCAGATGACATCCATCAAGAAACAGAGATCCCCAGATGATGAA 1224
Db
1021 CAGAACACACATGGTATTCAGATGACATCCATCAAGAAACAGAGATCCCCAGATGATGAA 1080
QY 1225 CTGTTATCTTACCAGTGTAGGGCGCTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1284
Db
1081 CTGTTATCTTACCAGTGTAGGGCGCTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1140
QY 1285 TCCTTGGAACCTCATGCACTACCTTCTCAGCACACAAATTTGAAACGCTACAGGCAACAGCAA 1344
Db
1141 TCCTTGGAACCTCATGCACTACCTTCTCAGCACACAAATTTGAAACGCTACAGGCAACAGCAA 1200
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Qy 1345 CAGCAGCAGCACCAGCAGCTTACTTCAGAAACA 1376
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Db 1201 CAGCAGCAGCACCAGCAGCTTACTTCAGAAACA 1232
|||||

Search completed: June 28, 2003, 10:09:12
Job time : 7013 secs

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:59:43 ; Search time 157 Seconds

(without alignments)

5500.648 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

Sequence: 1 tctgtgatatacaagacagt.....gcattcttggtttaaagaaa 2816

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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- 5: /cgn2_6/ptodata/2/ina/PCRS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2816	100.0	2816	4	US-09-643-597-333
2	1376	48.9	2270	4	US-09-643-597-332
3	1275	45.3	4849	4	US-09-643-597-335
4	1232	43.8	1551	4	US-09-643-597-337
5	1026	36.4	1386	4	US-09-643-597-336
6	975	34.6	2082	4	US-09-643-597-334
7	826	29.3	4655	4	US-09-643-597-151
8	822	29.2	2820	4	US-09-643-597-331
9	24	0.9	279	4	US-09-438-906-12
10	23	0.8	39	1	US-08-222-177A-86
11	23	0.8	40	1	US-08-222-177A-152
12	23	0.8	54	1	US-08-469-802B-27
13	23	0.8	54	2	US-08-267-803B-45
14	23	0.8	56	1	US-08-222-177A-149
15	23	0.8	66	1	US-08-469-802B-29
16	23	0.8	66	2	US-08-267-803B-47
17	23	0.8	155	1	US-08-222-177A-19
18	23	0.8	155	3	US-08-903-139B-11
19	23	0.8	155	3	US-08-903-139B-12
20	23	0.8	155	3	US-08-903-139B-13
21	23	0.8	155	3	US-08-903-139B-14
22	23	0.8	183	1	US-08-222-177A-20
23	23	0.8	283	4	US-08-118-200-11
24	23	0.8	283	4	US-08-458-745-11
25	23	0.8	318	1	US-08-222-177A-2
26	23	0.8	449	3	US-08-903-139B-16
27	23	0.8	564	1	US-08-117-362-32

c	28	23	0.8	564	1	US-08-486-924-32	Sequence 32, Appl
c	29	23	0.8	571	4	US-08-465-343A-2	Sequence 2, Appl
c	30	23	0.8	658	4	US-09-717-041-1	Sequence 1, Appl
c	31	23	0.8	1001	4	US-09-641-638-400	Sequence 400, App
c	32	23	0.8	1016	1	US-08-109-391A-3	Sequence 3, Appl
c	33	23	0.8	1016	1	US-08-459-019A-3	Sequence 3, Appl
c	34	23	0.8	1016	2	US-08-460-428A-3	Sequence 3, Appl
c	35	23	0.8	1016	3	US-08-458-860A-3	Sequence 3, Appl
c	36	23	0.8	1083	4	US-09-177-650-121	Sequence 121, App
c	37	23	0.8	1259	2	US-08-485-778-3	Sequence 3, Appl
c	38	23	0.8	1259	3	US-08-520-550A-3	Sequence 3, Appl
c	39	23	0.8	2271	3	US-08-903-139B-10	Sequence 10, Appl
c	40	23	0.8	3791	4	US-08-675-773B-3	Sequence 3, Appl
c	41	23	0.8	4221	4	US-09-651-656-22	Sequence 22, Appl
c	42	23	0.8	4221	4	US-09-650-855-22	Sequence 22, Appl
c	43	23	0.8	4550	4	US-09-103-863-35	Sequence 35, Appl
c	44	23	0.8	4718	3	US-08-936-135-9	Sequence 9, Appl
c	45	23	0.8	4733	3	US-08-936-135-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-643-597-333

Sequence 333, Application US/09643597

Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 333

LENGTH: 2816

TYPE: DNA

ORGANISM: Homo sapiens

US-09-643-597-333

Query Match 100.0%; Score 2816; DB 4; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACATTCACGGTGCCACCCCT	60
Db	1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACATTCACGGTGCCACCCCT	60
Qy	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120
Db	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120
Qy	121	AAGAAGATTATACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180
Db	121	AAGAAGATTATACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180
Qy	181	CCAGAGTTTCCAGCATATCTGGATTTTCTGGAACGCTATATCTTCAGTTCAGTCCGCC	240
Db	181	CCAGAGTTTCCAGCATATCTGGATTTTCTGGAACGCTATATCTTCAGTTCAGTCCGCC	240
Qy	241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGCACAAACAGATTGAGATT	300

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[illegible]

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RESULT 2
US-09-643-597-332
; Sequence 332, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 21021.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-332

Query Match      48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCGTTGATATCAAGACAGAGTGTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCCCT 60
      |||
Db      1 TCGTTGATATCAAGACAGAGTGTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCCCT 60

Qy      61 ACAGTACTGCCTCGACCTTACATCCACAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
      |||
Db      61 ACAGTACTGCCTCGACCTTACATCCACAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120

Qy      121 AAGAAAGTTATTACCGATCCACCATGTCCAGAGACACAGACAAATGAATTCCTCAGT 180
      |||
Db      121 AAGAAAGTTATTACCGATCCACCATGTCCAGAGACACAGACAAATGAATTCCTCAGT 180

Qy      181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTCAGTTCAGCCC 240
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FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 337
LENGTH: 1551
TYPE: DNA
ORGANISM: Homo sapiens
US-09-643-597-337

Query Match 43.8%; Score 1232; DB 4; Length 1551;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ATGTCCAGAGCAGACAGCAAAATGATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
DB 1 ATGTCCAGAGCAGACAGCAAAATGATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
QY 205 GATTTCTGGAACAGCCTATATGTTCACTTCCAGCCCATTTGACTTGAATTTGTGGATGAA 264
DB 61 GATTTCTGGAACAGCCTATATGTTCACTTCCAGCCCATTTGACTTGAATTTGTGGATGAA 120
QY 265 CCATCAGAAGATGGTGGCAAAACAGATTGAGATTAGCATGAGCTGTATCCGCATCAG 324
DB 121 CCATCAGAAGATGGTGGCAAAACAGATTGAGATTAGCATGAGCTGTATCCGCATCAG 180
QY 325 GACTCGAGCTGAGTACCCCATGTGGCCAGATGACAGCAACCTGGGGCTCCTGAAACAGC 384
DB 181 GACTCGAGCTGAGTACCCCATGTGGCCAGATGACAGCAACCTGGGGCTCCTGAAACAGC 240
QY 385 ATGACACAGCAGATTTCAGAACGGCTCCTGCTCCACCACTGCTTATACACAGACAGCAGC 444
DB 241 ATGACACAGCAGATTTCAGAACGGCTCCTGCTCCACCACTGCTTATACACAGACAGCAGC 300
QY 445 CAGAACAGCTGAGGGGGCCCTGCGCTACGACAGCCAGCTCCACTGCACTGACTC 504
DB 301 CAGAACAGCTGAGGGGGCCCTGCGCTACGACAGCCAGCTCCACTGCACTGACTC 360
QY 505 TCTCATCAGCCGCTATCCCTCCACACAGCTACCCAGCCGCGCAGCTTTCGACGTG 564
DB 361 TCTCATCAGCCGCTATCCCTCCACACAGCTACCCAGCCGCGCAGCTTTCGACGTG 420
QY 565 TCCTTCCAGCAGTGGACACCGCCAGTGGCCACCTGGAGCTTATCCACTGCACTGAA 624
DB 421 TCCTTCCAGCAGTGGACACCGCCAGTGGCCACCTGGAGCTTATCCACTGCACTGAA 480
QY 625 AAATCTACTGCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
DB 481 AAATCTACTGCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540
QY 685 CCTCAGGAGCTGTTATCCCGGCCATGCTGTCTACAAAAAGCTGACGACGTACCGAG 744
DB 541 CCTCAGGAGCTGTTATCCCGGCCATGCTGTCTACAAAAAGCTGACGACGTACCGAG 600
QY 745 GTGGTGAAGGGTGGCCCAACCATGAGTGGCGTGAATTCACAGAGGACAGATGTC 804
DB 601 GTGGTGAAGGGTGGCCCAACCATGAGTGGCGTGAATTCACAGAGGACAGATGTC 660
QY 805 CCTCCTAGTATTGATTCAGTAGAGGGGAACAGCCATGCCCATGTATGAGAGATCCC 864
DB 661 CCTCCTAGTATTGATTCAGTAGAGGGGAACAGCCATGCCCATGTATGAGAGATCCC 720
QY 865 ATCAGAGAGACAGATGCTGGTACCTTATGAGCCACCCAGCTTGGCACTGAATTC 924
DB 721 ATCAGAGAGACAGATGCTGGTACCTTATGAGCCACCCAGCTTGGCACTGAATTC 780
QY 925 ACAGACCTCTGTACAAATTTTCATGTGAACAGCAGTTGTGTGGAGGATGAACCGCGT 984
DB 781 ACAGACCTCTGTACAAATTTTCATGTGAACAGCAGTTGTGTGGAGGATGAACCGCGT 840
QY 985 CCAATTTTAATCATTTGTTACTCTGGAAACACAGATGGCAAGTCTTGGGGCCGACGTGC 1044
DB 1044 CCAATTTTAATCATTTGTTACTCTGGAAACACAGATGGCAAGTCTTGGGGCCGACGTGC

DB 841 CCAATTTTAATCATTTGTTACTCTGGAAACACAGATGGCAAGTCTTGGGGCCGACGTGC 900
QY 1045 TTTGAGGCCCGGATCTGTGCTTGGCCAGGAGACAGAGGCGGATGAGATGATGATC 1104
DB 901 TTTGAGGCCCGGATCTGTGCTTGGCCAGGAGACAGAGGCGGATGAGATGATGATC 960
QY 1105 AGAAAGCAGCAAGTTTCGGCAGCTACAAAGAACGGTGTATGTTAGAAAGCGCCCTTTGCT 1164
DB 961 AGAAAGCAGCAAGTTTCGGCAGCTACAAAGAACGGTGTATGTTAGAAAGCGCCCTTTGCT 1020
QY 1165 CAGAACACATGATGATCCAGATGACATCCATCAAGAAACGAGATCCCAAGATGATGAA 1224
DB 1021 CAGAACACATGATGATCCAGATGACATCCATCAAGAAACGAGATCCCAAGATGATGAA 1080
QY 1225 CTGTTATACCTACAGTGGGGCGCTGAGACTTATGAAATGCTGTTCAAGATCAAGAG 1284
DB 1081 CTGTTATACCTACAGTGGGGCGCTGAGACTTATGAAATGCTGTTCAAGATCAAGAG 1140
QY 1285 TCCCTGGAACCTATGCACTGACCTTCTCAGCACACAATTTGAAAGCTACAGGCAACAGCA 1344
DB 1141 TCCCTGGAACCTATGCACTGACCTTCTCAGCACACAATTTGAAAGCTACAGGCAACAGCA 1200
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376
DB 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232

RESULT 5

US-09-643-597-336
Sequence 336, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 336
LENGTH: 1386
TYPE: DNA
ORGANISM: Homo sapiens
US-09-643-597-336

Query Match 36.4%; Score 1026; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GCCACAGTACACGAACCTGGGGCTCCTGAACAGCATGGACCCAGCAGATTCAGAACGGCTC 410
DB 42 GCCACAGTACACGAACCTGGGGCTCCTGAACAGCATGGACCCAGCAGATTCAGAACGGCTC 101
QY 411 CTCGTCCACCACTCCCTATATACAGACACCGCCAGAACGCTGTCAGGGCCGCTCCGCC 470
DB 102 CTCGTCCACCACTCCCTATATACAGACACCGCCAGAACGCTGTCAGGGCCGCTCCGCC 161
QY 471 CTAGGCACACCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAA 530
DB 162 CTAGGCACACCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAA 221
QY 531 CACCGACTACCCAGGCCGCGACAGTTTCGAGCTGTCTTCCAGCAGTTCGAGCAGCGCA 590

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Db 222 CACCGACTACCCAGGCGCCGACAGATTTCGACGTTCTCCAGCAGTCGAGCAGCGCAA 281
Qy 591 GTGGCCACCTGGACGATTCCTGACTGAACGAACTCTACTGCCAATTCGAAGAC 650
Db 282 GTGGCCACCTGGACGATTCCTGACTGAACGAACTCTACTGCCAATTCGAAGAC 341
Qy 651 ATGCCCCATCAGATCAAGTGATGACCCCACTCTCTCAGGAGCTGTATTCGCGGCAT 710
Db 342 ATGCCCCATCAGATCAAGTGATGACCCCACTCTCTCAGGAGCTGTATTCGCGGCAT 401
Qy 711 GCCTGTCTACAAAAGCTGAGCAGCTGACGGAGGTGGTGAACGGTGCCCAACCATGA 770
Db 402 GCCTGTCTACAAAAGCTGAGCAGCTGACGGAGGTGGTGAACGGTGCCCAACCATGA 461
Qy 771 GCTGAGCCGTGAATTCACAGGAGGACAGATTGCGCTCTCTAGTCATTTGATTCGATGA 830
Db 462 GCTGAGCCGTGAATTCACAGGAGGACAGATTGCGCTCTCTAGTCATTTGATTCGATGA 521
Qy 831 GGGGACAGCCATGCCAGTATGTAGAGATCCCATCACAGGAAGACAGAGTGTCTGGT 890
Db 522 GGGGACAGCCATGCCAGTATGTAGAGATCCCATCACAGGAAGACAGAGTGTCTGGT 581
Qy 891 ACCTTATGAGCCACCCAGCTTGGCACTGAATTCAGCAGCTCTTGTACAAATTCATGTG 950
Db 582 ACCTTATGAGCCACCCAGCTTGGCACTGAATTCAGCAGCTCTTGTACAAATTCATGTG 641
Qy 951 TAACAGAGTGTGTGGAGGATGAACCGCGCTCCCAATTTAATCATTTGTACTCTGGA 1010
Db 642 TAACAGAGTGTGTGGAGGATGAACCGCGCTCCCAATTTAATCATTTGTACTCTGGA 701
Qy 1011 AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTGAGGCGCGGATCTGTGCTGGCC 1070
Db 702 AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTGAGGCGCGGATCTGTGCTGGCC 761
Qy 1071 AGGAAGACAGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 1130
Db 762 AGGAAGACAGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 821
Qy 1131 AAGAAGCGTGATGTGACGAAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGAC 1190
Db 822 AAGAAGCGTGATGTGACGAAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGAC 881
Qy 1191 ATCCATCAAGAAGCAAGATCCCGAGATGATGAACGTTTATCTTACAGTGAAGGGCGG 1250
Db 882 ATCCATCAAGAAGCAAGATCCCGAGATGATGAACGTTTATCTTACAGTGAAGGGCGG 941
Qy 1251 TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCACTTCTTCC 1310
Db 942 TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCACTTCTTCC 1001
Qy 1311 TCAGCACAAATTTGAACGCTACAGGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGTTC 1370
Db 1002 TCAGCACAAATTTGAACGCTACAGGCAACAGCAAGCAGCAGCAGCAGCAGCAGCAGTTC 1061
Qy 1371 GAAACA 1376
Db 1062 GAAACA 1067
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RESULT 6

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US-09-643-597-334
; Sequence 334, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
```

```
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-334
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Query Match 34.6%; Score 975; DB 4; Length 2082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1025; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 477 GCCACAGTACAGAACTCGGGCTCCTGAACAGCATGGACCAGCATTCAGAACCGCTC 536
Qy 411 CTCGTCCACAGTCCCTATTAACACAGCACGCGCAGAAAGCGTCCACGCGCCCTCGCC 470
Db 537 CTCGTCCACAGTCCCTATTAACACAGCACGCGCAGAAAGCGTCCACGCGCCCTCGCC 596
Qy 471 CTACGACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA 530
Db 597 CTACGACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA 656
Qy 531 CACCGACTACCCAGGCGCCGACAGTTTCGACGTTGCTTCCAGCAGTCCAGCAGCCCAA 590
Db 657 CACCGACTACCCAGGCGCCGACAGTTTCGACGTTGCTTCCAGCAGTCCAGCAGCCCAA 716
Qy 591 GTCGGCCACTCGGACGTTATCCACTGAACGAACTCTACTGCCAATTCGAAAGAC 650
Db 717 GTCGGCCACTCGGACGTTATCCACTGAACGAACTCTACTGCCAATTCGAAAGAC 776
Qy 651 ATGCCCCATCCAGATCAAGTGATGACCCCACTCTCTCAGGAGCTGTTATCCGCGCCAT 710
Db 777 ATGCCCCATCCAGATCAAGTGATGACCCCACTCTCTCAGGAGCTGTTATCCGCGCCAT 836
Qy 711 GCCTGTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGA 770
Db 837 GCCTGTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGA 896
Qy 771 GCTGAGCCGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCATTTGATTCGAGTAGA 830
Db 897 GCTGAGCCGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCATTTGATTCGAGTAGA 956
Qy 831 GGGGAAACGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGCAGAGTGTCTGGT 890
Db 957 GGGGAAACGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGCAGAGTGTCTGGT 1016
Qy 891 ACCTTATGAGCCACCCAGGTTGGCAGTGAATTCACAGAGCTCTTGTACAAATTCATGTG 950
Db 1017 ACCTTATGAGCCACCCAGGTTGGCAGTGAATTCACAGAGCTCTTGTACAAATTCATGTG 1076
Qy 951 TAACAGAGTGTGTGGAGGATGAACCGCGTCCCAATTTAATCATTTGTACTCTGGA 1010
Db 1077 TAACAGAGTGTGTGGAGGATGAACCGCGTCCCAATTTAATCATTTGTACTCTGGA 1136
Qy 1011 AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTCAGGCGCGGATCTGTGCTTGGCC 1070
Db 1137 AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTCAGGCGCGGATCTGTGCTTGGCC 1196
Qy 1071 AGGAAGACAGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 1130
Db 1197 AGGAAGACAGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 1256
Qy 1131 AAGAAGCGTGTGTGTCAGAAAGCGCCCTTTCGTGAGAACACACATGGTATCCAGATGAC 1190
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Qy	951	TAAACAGCAGTTGTGTTGGAGGGATGAACCGCGCTCAATTTTAAATCATTTGTTACTCTGGA	1010
Db	764	TAAACAGCAGTTGTGTTGGAGGGATGAACCGCGCTCAATTTTAAATCATTTGTTACTCTGGA	823
Qy	1011	AACCAGAGATGGGCAAGTCTCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCC	1070
Db	824	AACCAGAGATGGGCAAGTCTCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCC	883
Qy	1071	AGGAAGAGACAGGAAGCGCGATGAAGATAGCATCAGAAGACAGCAAGTTTCGGGACAGTAC	1130
Db	884	AGGAAGAGACAGGAAGCGCGATGAAGATAGCATCAGAAGACAGCAAGTTTCGGGACAGTAC	943
Qy	1131	AAAGAACGGTGATGGTACGAAGCCCGCTTTGTCGACAAACACACATGGTATCCAGATGAC	1190
Db	944	AAAGAACGGTGATGGTACGAAGCCCGCTTTGTCGACAAACACACATGGTATCCAGATGAC	1003
Qy	1191	ATCCATCAAGAAACGAAGATCCCCAGATGATGAAC	1227
Db	1004	ATCCATCAAGAAACGAAGATCCCCAGATGATGAAC	1040

RESULT 8
US-09-643-597-331
; Sequence 331, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun

```

: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF LUNG CANCER
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 331
: LENGTH: 2820
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-643-597-331

```


IMMEDIATE SOURCE:
CLONE: mfd12rs
US-08-222-177A-86

Query Match 0.8%; Score 23; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 36 GTGTGTGTGTGTGTGTGTGTG 14

RESULT 11

US-08-222-177A-152/c
Sequence 152, Application US/08222177A
Patent No. 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (GC-GA)n (GG-GT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/222,177A
APPLICATION NUMBER: 435
FILING DATE: 21-APR-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 152:

SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd34rs
US-08-222-177A-152

Query Match 0.8%; Score 23; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 24 GTGTGTGTGTGTGTGTGTGTG 2

RESULT 12

US-08-469-802B-27/c
Sequence 27, Application US/08469802B
Patent No. 5741645

GENERAL INFORMATION:

APPLICANT: Ori, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghdi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/469,802B
APPLICATION NUMBER: 435
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Muetling, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00030101

TELEPHONE: 612-305-1217

TELEFAX: 612-305-1225

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-469-802B-27

Query Match 0.8%; Score 23; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 47 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 13

US-08-267-803B-45/c

Sequence 45, Application US/08267803B

Patent No. 5834183

GENERAL INFORMATION:

APPLICANT: Ori, Harry T.

APPLICANT: Ranum, Laura P.W.

APPLICANT: Chung, Ming-yi

APPLICANT: Zoghdi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosis

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.

STREET: P.O. Box 581415

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55458-1415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-45

Query Match 0.8%; Score 23; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
|||||
DB 47 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 14

US-08-222-177A-149/c
Sequence 149, Application US/08222177A
Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
(d-c-a)n.(d-g-tt)n SEQUENCES AND METHODS OF USING SAME

TITLE OF INVENTION: (d-c-a)n.(d-g-tt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562

FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 09865.601

TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100

TELEFAX: (608) 831-2106

TELEX:
INFORMATION FOR SEQ ID NO: 149:

SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd33rs
US-08-222-177A-149

Query Match 0.8%; Score 23; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
|||||
DB 44 GTGTGTGTGTGTGTGTGTGTG 22

RESULT 15

US-08-469-802B-29

Sequence 29, Application US/08469802B

Patent No. 5741645

GENERAL INFORMATION:
APPLICANT: Orr, Harry T.

APPLICANT: Rannum, Laura P.W.

APPLICANT: Chung, Ming-yi

APPLICANT: Zoghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5741645

TITLE OF INVENTION: Type 1 and Method for Diagnosis

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.

STREET: 119 No. 5741645th Fourth Street, Suite 203

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Muetting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00030101

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217

TELEFAX: 612-305-1225

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA
US-08-469-802B-29

Query Match 0.8%; Score 23; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
|||||
DB 41 GTGTGTGTGTGTGTGTGTGTG 63

Search completed: June 28, 2003, 11:10:35
Job time: 159 secs

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IMMEDIATE SOURCE:
CLONE: mfd12rs
US-08-222-177A-86

Query Match 0.8%; Score 23; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 36 GTGTGTGTGTGTGTGTGTGTG 14

22 nks

RESULT 11

US-08-222-177A-152/c
Sequence 152, Application US/08222177A
Patent No. 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 152:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: mfd34rs

US-08-222-177A-152

Query Match 0.8%; Score 23; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 24 GTGTGTGTGTGTGTGTGTGTG 2

RESULT 12

US-08-469-802B-27/c
Sequence 27, Application US/08469802B
Patent No. 5741645

GENERAL INFORMATION:

APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muetting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-469-802B-27

Query Match 0.8%; Score 23; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568
DB 47 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 13

US-08-267-803B-45/c

Sequence 45, Application US/08267803B
Patent No. 5834183

GENERAL INFORMATION:

APPLICANT: Orr, Harry T.

APPLICANT: Rannum, Laura P.W.

APPLICANT: Chung, Ming-yi

APPLICANT: Zoghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosis

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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Creation date: 09-22-2004
Indexing Officer: BHULUKA - BEKANA HULUKA
Team: OIPEBackFileIndexing
Dossier: 09670568

Legal Date: 07-07-2003

No.	Doccode	Number of pages
1	SRNT	4

Total number of pages: 4

Remarks:

Order of re-scan issued on

